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Jan 27 14:04:07 2003
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Title:
Perfect score:
Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Scoring table: OM protein - protein search, using sw model Database Searched: Run on: number of hits satisfying chosen parameters: SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungl:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi
15: sp_bacteriap:
16: sp_bacteriap:* January 24, 2003, 19:40:10; Search time 35 Seconds (without alignments) 2095.794 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-675-509-4
1802
1 MSTQPKTLTVGLFPYLPSWN......CVDFANKEVKNCAGVLRPFL 356 671580 seqs, 206047115 residues sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_bhage:*
sp_plant:*
sp_value:*
sp_value:*
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sp_value:*
sp_value:*
sp_value:*
sp_bacteriap:*
sp_archeap:* GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. sp_human:*
sp_invertebrate:* 671580

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	, 12	11	10	9	8	7	0	ű	4.	ω	2	μ.	Result No.
106.5	106.5	107	108	108.5	109	110.5	110.5	111	111.5	111.5	112.5	114.5	115	116	118.5	Score
5.9	5.9	5.9	6.0	6.0	6.0	6.1	6.1	6.2	6.2	6.2	6.2	6.4	6.4	6.4	6.6	Query
1033	1007	2081	528	998	448	912	718	417	1414	613	1360	1431	286	1248	345	Length
10	9	17	s	v	10	H	10	16	17	17	ഗ	v	N	10	16	BB
Q9CAA7	Q9F4J3	Q9HJ37	Q20730	044800	024399	070410	Q94JF5	Q8RBL7	Q8TH79	Q97YF0	015807	Q9XYH6	Q9RLV6	Q9SAJ2	QBRD78	Ħ
Q9caa7 arabidopsis	Q9f4j3 streptococc	Q9hj37 thermoplasm	Q20730 caenorhabdi	O44800 caenorhabdi	O24399 triticum ae	0	Q94jf5 oryza sativ	Q8rb17 thermoanaer	Q8th79 methanosarc	Q97yf0 sulfolobus	O15807 cryptospori	Q9xyh6 cryptospori	Q9rlv6 lactococcus	Q9saj2 arabidopsis	Q8rd78 thermoanaer	Description

4 5	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
101.5	101.5	101.5	101.5	102	102.5	102.5	103	103	103	103	103	103.5	103.5	103.5	104	104.5	104.5	104.5	104.5	105	105.5	105.5	105.5	106	106	106	106.5	106.5
5.6	5.6	5 6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5. 8	5.8	5. 8	5. 8	5. 8		5.9			5.9	5.9	5.9	5. 9	5.9
767	728	703	505	578	704	598	2701	1857	738	637	286	4643	1733	692	689	2806	2462	628	503	1058	1277	602	358	1220	1054	545	2819	1166
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Q94543	Q9M9S4	Q93MA0	Q93335	Q9SDM7	031399	Q9L746	Q8WN96	Q8TGC5	Q9AQF4	Q92DW5	Q9CIN5	Q9VW71	Q8TTS9	Q97YM6	Q8RSZ0	Q8RI19	Q8RGZ3	Q9PQ47	Q97XR3	Q9I943	050698	Q8RBX6	Q928M1	Q9P3A8	Q9PR50	Q9V283	Q98QP8	Q8V7K1
Q94543 drosophila	Q9m9s4 arabidopsis	Q93ma0 clostridium	Q93335 caenorhabdi	J	O31399 bacillus su	Q91746 haemophilus			Q9aqf4 clostridium	Q92dw5 listeria in	Q9cin5 lactococcus	Ω	Q8tts9 methanosarc	Q97ym6 sulfolobus	Q8rsz0 pseudomonas	Q8ri19 fusobacteri	_		Q97xr3 sulfolobus	Q9i943 carassius a	O50698 borrelia bu	Q8rbx6 thermoanaer	Q928ml listeria in	8	0		-	Q8v7k1 chlorella v

ALIGNMENTS

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/ 128 GTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLYQQLLQ 169	101 RTYALAKEVALGGKGCDLHEGVDVCTDPE 129	71FLPYLYSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFDQYLCSNFLLSSPN 127	41 EGGKSVKLDKLPSYEVIRVFITNQNKIEEMQLEDYVKGVVAAEMPAEFEIEALKAQAVAA 100	21 ENGNEVKLINLIK-DVLPTQVSGYN-IEYTEFDCYSDASLQS-LPDVFSTDSI 70	Query Match 6.6%; Score 118.5; DB 16; Length 345; Best Local Similarity 21.3%; Pred. No. 3; Matches 73; Conservative 60; Mismatches 118; Indels 91; Gaps 17;	SEQUENCE	<pre>V Complete proteome.</pre>	Genome Res. 12:689-700(2002).	"A complete sequence of T. tengcongensis genome.";	Chen r., Aue r., Au r., Lai A., Huang	Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.	MEDLINE=21992816;	SEQUENCE FROM N.A.			Thermoanaerobacteriales; Thermoanaerobacteriaceae	: Thermoanaerobacter tengcongensis. Thermoanaerobacter tengcongensis.	SPOIID OR TTEO168.	Sporul	01-JUN-2002 (TrEMBLrel. 21, Last	01-JUN-2002 (TrEMBLrel. 21,	QBRD78; 01-JUN-2002 (TrEMBLrel.		

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Q9SAJ2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00109; TYKKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Transferase; Tyrosine-protein_kinase.

ATP-binding; Transferase; Tyrosine-protein_kinase.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk pkinase.
InterPro; IPR004040; STY pkinase.
InterPro; IPR001245 Ty pkinase.
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T8K14.1.
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                                                                                                                                                                                                                    MNYNTGYMELRGLIGISHTGSECASDVSRFSTVENGTSDIERTNSSLHEFGNKLNHVQSA 145
                                                                                                                                                                                                                                                                                     -GYNIEYTEF
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Best Local S
Matches 47
                                             Q9XYH6;
Q9XYH6;
01-NOV-1999
01-NOV-1999
01-JUN-2002
ATP-binding
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Q9RLV6;
01-MAY-2000
            CPABC.
Cryptosporidium parvum.
Eukaryota; Alveolata; P
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MEDLINE=20112344; PubMed=10647818;
Aungpraphapornchai P., Griffin H.G., Gasson
"Cloning, DNA sequence analysis, and deletio
diacetyl-acetoin reductase from Lactococcus
DNA Seq. 10:163-172(1999).
Eukaryota; Alveolata;
Cryptosporidiidae; Cry
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                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004872; Lipoprotein_9.
Pfam; PF03180; Lipoprotein_9; 1.
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                                                                                                                                                                                         NKDITOKYRTILDSTVVASQREYINSVKQGKP
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                                                                                                                                                                                                                                                                                                                                 FPYLPSWNE--NGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ012388; CAB59827.1; -
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                                            (TrEMBLrel. 12, Cr
(TrEMBLrel. 12, La
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cassette protein.
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 21, Last annotation)
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 Cryptosporidium
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             Apicomplexa;
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Last sequence
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Pred. No. 3.9;
12; Mismatches
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                                                          sequence update) annotation updat
             Coccidia;
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deletion of a cocccus lactis.
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Best Local
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01-JAN-1998
01-MAR-2002
01-JUN-2002
STRAIN=KSU-1;
MEDLINE=97376910;
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PROSITE; PS00211; ABC TRANSPORTER; 2.
ATP-binding; Transport.
SEQUENCE 1431 AA; 162177 MW; 18AB.
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Perkins M.E., Riojas Y.A., Wu T.W., Le Blancq S.M.;
"CPABC, a cryptosporidium parvum ATP-binding cassette
host-parasite boundary in intracellular stages";
Proc. Natl. Acad. Sci. U.S.A. 96:5734-5739(1999).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                             SEQUENCE FROM N.A.
                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Cryptosporidiidae; Cryptosporidiidae;
                                                                                                                                                                     Cryptosporidium
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InterPro; IPR003439; ABC_transportx.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_tran; 2.
SMART; SM00382; AAA; 2.
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                                                                                                                                                                                                                cassette protein
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  PubMed=9233681;
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Pred. No. 42;
61; Mismatches
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01-OCT-2001
01-OCT-2001
01-OCT-2001
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SEQUENCE
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                     Sulfolobus solfataricus Archaea; Crenarchaeota;
                                                                   Hypothetical SSO1375.
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Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transport
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  Sulfolobus
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l protein SSO1375.
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61; Mismatches
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Q1-JUN-2002 (TrEMBLrel. 21, Li
Q1-JUN-2002 (TrEMBLrel. 21, Li
Q1-JUN-2002 (TrEMBLrel. 21, Li
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STRAIN=C2A / ATCC
MEDLINE=21929760;
Galagan J.E., Nush
                                                                                                      Hypothetical
MA4643.
                                   SEQUENCE
                                                                    Archaea; Euryarchaeota; Methanococo
Methanosarcinaceae; Methanosarcina
                                                                                         Methanosarcina acetivorans
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EMBL; AE006751; AAK41609.1; -.
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                                                       NCBI_TaxID=2214;
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613 AA; 67767 MW; F478840A4CCB9BA3 CRC64;
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01-JUN-2002
                     Bao Q., Tian Y., Li W., Xu Z., Xuan Z., H
Chen Y., Xue Y., Xu Y., Lai X., Huang L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis
Genome Res. 12:689-700(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sugar-binding pour UGPB OR TTE0799
                                                                                                                                                                      STRAIN=MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQSSSSA-----AVDIKASDLPQSGDQVNKD---ITQKYRTILDSTVVASQREYINSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSHETEEYNKTESYRLLYTVLVDGIDITLAQ----EEVLGSSSAEVSEDLVLAEEYYQNI
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AE013046;
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1414 AA; 1
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Pred. No. 65;
56; Mismatches
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                                                                                                               Dong X., N
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                                                                                                                                                                                                                                                                                                                     STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0648B02.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003023; BAB44026.1;
InterPro; IPR001644; CBS domain.
InterPro; IPR001807; C1-Channel_volt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q94JF5;
                                                                                                                                                                                                                                                              Pfam; PFO
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                             Pram;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice)
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                                                                                               55 DASLQSLPDVFSTDSIFLPYLYSLGGYKSLDESLVR--GVTGDLHSFVSSSASVNGSVYG 112
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FPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLYQQLLQSSS
                                                  DILLESRP---FTSGLSAAVLVQLIGVKVLATSLCRAFGLVGGYYAPSLFIGAATGMAYG
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                                                                                                                                                                                                                                                      PF00571; CBS; 2.
PF00654; voltage_CLC; 1.
NCE 718 AA; 76362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSSNF----YAQLSQQFDAKESEV-----RVLRCVDFANK 343
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                                                                                                                                                         36;
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                                                                                                                                                    Score 110.5;
Pred. No. 29;
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Pred. No. 13;
8; Mismatches 143;
                                                                                                                                                                                                                                                           DAB54F202012785B CRC64;
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                                                                                                                                                                                                      DB 10; Length
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                                                                                                                                                      Gaps
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RESULT
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Best Local :
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Ryba N.J.P., Tirindelli R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF053986; AAC08413.1; -.
InterPro; IPR001828; ANF receptor.
InterPro; IPR001828; ANF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Putative pheromone receptor V2R2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97436753; PubMed=9292726;
Ryba N.J., Tirindelli R.;
"A new multigene family of putative
Neuron 19:371-379(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              070410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=VOMERONASAL NEURONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                               EYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKDPNDVLTIEFWQTAFNCTWPNSSVPYN
                                                NYY-----VGYSESMCEI---KDIIRDQQ
                                                                                                                                                                                             SEAIVNLIKHFGW--VWVGAIAADDDYGKYGVKTFKEKMESANLCVAFSETIPKVYSNEK 263
                                                                                                                                                                                                                                              ASSLLELAQKVGYEQIVYPDVASSSSFTVFGL--YQQLLQSS-----
                                                                                                                                                                                                                                                                                                 AALVGSGGSSLSVAASRILGLYYMPQVGYTSSCSILSDKFQFPSY----LRVLPSDNLQ
                                                                                                                                                                                                                                                                                                                                               PYLVSLGGVK-SLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQ 131
                                                                                                                                                                                                                                                                                                                                                                                                IKEINERKDILPNHTLGYQI----FDSCYTISKAMESSLVFLTGQEEFKPNFRNSTGSTL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QENLTVAEAMKTKY I SVSKTTPVVEALNLML
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                                                                                                 MQKAVKAVKTSTAKVIVLYTSDIDLSLFVLEMIHHNITDRTWIATE-AWITSALIAKP--
                                                                                                                                               PQSGDQVNKDITQK--------YRTILDSTVVASQREYINSVKQGKPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VAVEVIK----NLLTNTLVLDLLGLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                912 AA;
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ilarity 21.0%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102348 MW;
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Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110.5;
Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Best Local
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00307; CH; 'SMART; SM00033; CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. VICTORY; TISSUE=ROOT;
MEDLINE=97422889; PubMed=9276954;
Cruz-Ortega R., Cushman J.C., Ownby J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fimbrin/plastin-like (Fragment).
Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CDNA clones encoding 1,3-beta-glucanase and a fimbrin-like Cytoskeletal protein are induced by Al toxicity in wheat roots.";
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lant Physiol. 114:1453-1460
MBL; U67717; AAC49813.1; -.
SSP; P13797; 1AOA.
                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                               VYGF-----PQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYP-DVASSSSFTVFG
                                                                                                                                 GKPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAV
                                                                                                                                                                                 LYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQK---YRTILDSTVVASQREYINSVKQ
                                                                                                                                                                                                                                                                                  LPDVFS--TDSIFLPYLVSLGGVKSLDESLVR------
                                                                                                                                                                                                                                                                                                          LNPWERNENHTLCLNSAKAIGCTVVNIGTQFLVEGRPHLVLGLISQIIKIQLLADLNLKK 64
                                                                                                                                                                                                                                                                                                                                  LRCVDFANKEVK 346
                                                                                  EV---IKNLLTNTLVL--DLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRV
                                                                                                                                                         FVAQIFQHRNGLTSDIKQVTLTQSASRDDVLVSREERAFRMWINSLGVES---YLNNVFE
                                                                                                                                                                                                          AYAYLLKALAPE-TSPETTLETKNPDERAKMVLEQAEKLDCKRYLTPKDITEGSANLNLA
                                                                                                                                                                                                                                                            TPQLVELFDDSKDIDEVLSL----
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                                                        ELKFSLVNLAGNDIVQGNKKLIVALLWQLMRFNILQLLNRLRSHSKGSQGKQITDADI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LPANKNGIAHLAK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLT---
                                                                                                           -DVRNGWV----LLEVLDKVSPGSVNWKL--
                                                                                                                                                                                                                                                                                                                                                                        Similarity
            LNWANSKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50021; CH;
                                                                                                                                                                                                                                                                                                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            AA,
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                                                                                                                                                                                                                                                                                                                                                                                                            50505 MW;
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Pred. No. 19;
72; Mismatches
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Last
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                                                                                                                                                                                                                                                          -STEKMLLRWMNHHLKKAGYKKTVNNF--SSDVKDGE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLCTGEEK--LEDLKN----TYLDTSQLRITKQC 427
                                                                                                                                                                                                                                                                                                                                                                                                            3C0A39B8DAA808C7
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                                                                                                          ESKPPIKLPFRKLEN--CNQVVKIGK
                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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                                                                                                                                                                                                                                                                                  GVTGDLHSFVSSSASVNGS 109
                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                          68;
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RESULT 12
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STRAIN-BRISTOL N2;
Du Z., Le T.T.;
"The sequence of C. e
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         044800;
044800;
01-JUN-1998
01-JUN-1998
01-JUN-2002
F14D2.6 prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favelo A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roppra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1997) to the EMBL/Gei
EMBL; AF040643; AAB94960.1; -.
InterPro; IPR000494; EGFR L domain.
Pfam; PF01030; Recep L domain; 3.
SEQUENCE 998 AA; Il3094 MW; BE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F14D2.6. Caenorhabditis elegans. Caenorhabditida; Rhabditoidea; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston
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                                                                                                                                                                                                                                                                                                                                            118
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VYTD--VLALNSN----
                                                       NEEYILNLKNTKVICGFGFFGAFGASCYFGERYGDIPLIRFSSNKLLRNVTLPQMKNPPF
                                                                                                               QREYINSVKQGKPISNY-YVGYSESMCEIKD-----
                                                                                                                                                                                                                               LQSSSSAAVDIKASDLPQSGDQVNKDITQK----
                                                                                                                                                                                                                                                                                    SFNFTSIHDNPN------LRRLGLDSL--KQLGPAGKFTIHIANNHPDFCLSTSE
                                                                                                                                                                                                                                                                                                                                            CSNF--LLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTV-----
                                                                                                                                                                                                                                                                                                                                                                                                       STTTQFPTIQTALQYLSSLSLLKKLNGMLEIYETGLENVSFLGNLETHNGKNGGLPEKYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTG-DLHSFVSSSASVNGSVYGFPQ-YL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTSIYNSIDWWSQETSKWDIINNTKLDVGIVCRVAERDI-YADFNAYGNRKVVAADSYK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTVGLFPYLPSWNENGNEVKLINLIK-DV-LPTQVSGYNIEYTEFDCYSDA-----SLQ
                                                                                                                                                                          LQVFARTNLKIYGFEV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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) to the
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  --LCDEKQKVAVEVIK 283
                                                                                                                                                                       QICKDLFRKDGQKTCIFKDLSMLDPKCQHIIGDIFINAT
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Last sequence update)
Last annotation update)
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108.5;
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BE48A4E614F90D1B
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RESULT 14
Q9HJ37
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    RROCCOS GETTTA
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Best Local
                                                                                                                                                                                                                                                    О9НJ37
О9НJ37;
                                                              TAIIJo.
Thermoplasma acidophilum.
Thermoplasma acidophilum.
                                                                                                                                                         01-MAR-2001 (TYEMBLIEL 16, Crea
01-MAR-2001 (TYEMBLIEL 16, Last
01-MAR-2001 (TYEMBLIEL 16, Last
01-MAR-2001 (TYEMBLIEL) 16, Last
Conserved hypothetical membrane
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
SCHOLT 277663; CAB01214.1; -
InterPro, IPR00960; Flav cont_mnoxgn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q20730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                            446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKDIIRDQQYN-----VQLIGTSDKPYVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLDESLVRG----VTGDLHSFVSSSASVNGS------VYGFPQYLCSNFLLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDVQL--FSRYYDTLLKTIPHAVAND--FMEYRLQQRMDHDVYGLRPDHRFFQQHPTVND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00743; FMO-
NCE 528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 6.0%;
l Similarity 21.7%;
59; Conservative 4
FROM N.A.
                                                                                                                                                                                                                                                                            PRELIMINARY;
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AA; 60119 MW;
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Last annotation updat
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Pred. No. 28;
47; Mismatches
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Bensing B.A., Rubens C.E., Sullam P.M.;
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      Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones H., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stelfon J., Simmonds M., Squares R., Stevens K., Sharp S., Stevens K., Simmonds M., Squares R., Stevens K., Sharp S.
                                                                                                                                                                                                                                                                                                                             15.JUN-2002 (Rel. 33, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Putative translational activator C18G6.05C (G
SPAC18G6.05C.
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Pfam; PF000427; PBS_linker_poly; 3.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 2.
ProDom; PD000340; Phycobilisome; 2.
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Q10105;
                                                                                                                                                                                      STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
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01-FEB-1996
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Phycobilisome; Electron transport; Photosynthesis;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
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Pred. No. 1.6
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"The genome sequence of Schizosaccharomyces pombe.";
"Instruction of Schizosaccharomyces pombe.";
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Weltjens I.,
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183 LPQSGDQVNKDITQKYRTILDS--TVVASQREYINSVKQGKPISNYYVGYSESMCE--IK 238
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01-FEB-1996 (R
Phycobilisome
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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P28561
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                                                                                                                                                                                                                                              Pfam; PF00427; PBS_linker_poly; 3.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 2.
                                                                                                                                                                                                                                                                                        HSSP; P00315; 1B33.
InterPro; IPR001297; PBS_linker_poly.
InterPro; IPR001659; Phycobilisome.
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                                                                                                                                                                                                                 Phycobilisome; Electron transport; Photosynthesis; Repeat; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                 EMBL; Z11905; CAA77957.1; -.
                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                  PIR; S20621; S20621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phycobiliprotein subunit genes from Aglaothamnion neglectum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization and transcript
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 157 SFTVFG---
                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMIN ENERGY ACCEPTOR AND AS A LINKER POLYPEPTIDE THAT STABILIZE THE PHYCOBILISOME ARCHITECTURE.

SIMILARITY: OF THE REPEATED DOMAINS TO N-TERMINAL REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHYCOCYANIN ROD LINKER POLYPEPTIDES
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                            SSVFRSLYWEPLYICKAIEYIHYRLLGRPSYGRQEINQYFDIVYREGYYKMIDYLLNSSE 636
                                                       ASVNGSVYGFPQYLCSNF-----
                                                                                     FSDEVMSLPPDIEQIIKAIYLRVFGRFIYLEELSSVRKF-ESLFRSSKISVRDFIRNLVK 576
                                                                                                                YSDASLQSLPDVFS-TDSIFLP-----YLVSLGGVKSLDESLVRGVTGDLHSFVSS--S
                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodophyta;
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                                                                                                                                                                                                    885 AA;
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rel. 24, Created)
Rel. 24, Last sequence update)
Rel. 33, Last annotation update)
linker polypeptide (Anchor poly)
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                                                                                                                                                                                                     101153 MW;
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                                                                                                                                            Score 108; DB
Pred. No. 5.5;
70; Mismatches
                                                     -LLSSPN-GTQQASSLLELAQKVGYEQIVYPDVASSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                     C91D75CD6307B4B9 CRC64;
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---LYQQLLQSSSSAAVDIKASDL---PQSGDQV 190
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                                                                                                                                              119;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 26077 / CBS 2863;

MEDLINE=92307400; PubMed=1612414;

MEDLINE=92307400; PubMed=16124
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"The nucleotide igene.";
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P19269;
01-NOV-1990
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FEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 26076;
MEDLINE=90032659;
                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no ways and the summer of the state of the same of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE=92120467; Pu
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Ol-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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AS THE ALPHA-AMYLASE FAMILY.
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ungi; Ascomycota; Saccharomycotina; Saccharomycetes
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      statement
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Hvdrolase; Glycosidase; Carbohydrate metabolism;
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X16040; CAA34162.1;
X62079; CAA43995.1;
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to license@isb-sib.ch).
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15-JUN-2002 (Re
15-JUN-2002 (Re
Cyclic di-GMP |
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Spiers A.J., Kahn S.G., Bohannon J., Travisano M., Raine
"Adaptive divergence in experimental populations of Pseu
"Iluoracems. I. Genetic and phenotypic bases of wrinkly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellulose biosynthesis.
SEQUENCE 689 AA; 752
                                          Isoleucyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics 161:33-46(2002).
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PATHWAY: Bacterial cellulose biosynthesis.
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                                                                                                                                                                                                                                                                                                                        FVSSSASVNGSVYGFPQYL----CSNFLLSSPNGTQQASSLLELAQKVGYEQ------
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                                                                                                                                                                                                               POSGDO------VNKDITQKYRTILDSTVVASQREYINS
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gw. Lathigra R., White O., Ketchum K.D., Richardson D., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch Ismith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG. Aminoacyl-tRNA synthetase; Protein biosynthesis; Metal-binding; Zinc; Complete proteome.
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InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002301; tRNA-synt_11e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                        Query Match
Best Local
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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Hori H., Suzuki N., Ogiwara K., Himejir
Minami M., Asano S., Sato R., Obba M.,
"Characterization of larvicidal toxin I
                                                                                                                                                                                                                                                                                                                                                                     Hori H., Asano S., Ohba M., Iwahana H.,
"Cloning, heterologous expression, and localization of a novel crystal
protein gene from Bacillus thuringiensis serovar japonensis strain
buibui toxic to scarabaeid insects.";
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                                                                                                                                                                                                                                                      thuringiensis serovar japonensis
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Bacteria; Firmicutes; F
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                                                                                                                                                                                                                                           scarabaeid beetles.";
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                                                                                                                                                                     Appl. Bacteriol. 76:307-313(1994).

FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MI FUNCTION: PROMOTES COLLOIDOSMOTIC ON VARIOUS SCARABAEID BE EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BE SUCH AS ANOMALA CUPREA, A. RUFOCUPREA AND POPILLIA JAPONICA. DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS RODUCED DURING
                ween the Swiss Institute of Bioinformat
Buropean Bioinformatics Institute. The
by non-profit institutions as long
ified and this statement is not removed.
                                                                                                    SIMILARITY:
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(Rel. 39, Last annotation update)
crystal protein cry8Ca (Insecticidal delta-endotoxin
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KIP1 OR CIN9 OR YBL063M OR YBL0504 OR YBL0521.
MEDLINE=94205266; PubMed=8154187; Scherens B., el Bakkoury M., Vierendeels F., Dub "Sequencing and functional analysis of a 32,560 left arm of yeast chromosome II. Identification frames, including the KIP1 and SEC17 genes."; Yeast 9:1355-1371(1993).
                                                                                        SEQUENCE FROM N.A.
STRAIN=S288C;
                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharor
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                                                                                                                                                                                MEDLINE=92317166;
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nilarity 22.6%;
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P.B., Rose M.D.;
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eins required
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Pred. No. 3
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EMBL; Z23261; CAA80785.1; -.
EMBL; Z35824; CAA84883.1; -.
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00073; HPT; 1.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us
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Cell 70:451-458(1992)
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STRAIN=S288c;
MEDLINE=92354062; PubMed=1643659;
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InterPro; IPR002570; Hpt.
InterPro; IPR001752; kinesin_motor.
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HSSP; P17119; 3KAR.
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SUBCELLULAR LOCATION: SPINDLE MICROTUBULES THAT LIE BETWEEN TH POLES.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
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NVLIENQQSGSSKLIKEQDLEIKKLKNDLINERRISNQFNQQL--AEMKRYFQDHVSRTR
                         ---ISNYYVGYS---
                                                QSDSTSHYRKDLNEIYQSHQQFLKNLQNDIKSCLDS-IGSSILTSINEISQNCTTNLNSM
                                                                        QSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKP-----
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COLLED COIL (POTENTIAL).
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                97.5;
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                                                                                                                                                                                                                                                                                 BB
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                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Coiled
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                                                                                                                                                                                                                                                                                Length 1111;
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L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
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IP3S_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                014571; U94', ),
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inssitol 1,4,5-trisphosphate receptor type 2 (Ty
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE=94361219; PubMed=8081734;
Yamamoto-Hino M., Sugiyama T., Hikiti
Hasegawa K., Sekine S., Sakurada K., M
Hasegawa M., Mikoshiba K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IP3S_HUMAN
Q14571; 09
                                                                                                                                                                                                                                                                      ++
                                                                    Genew;
                                                                                 EMBL; AB012610; BAA33961.1;
                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recept.
                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of 1,4,5-trisphosphate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
     InterPro;
                 [nterPro;
                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                          DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-
EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS TH
BINDING SITE IN THE N-TERMINAL AND MODULATORY SITES IN TH
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
MISCELLANBOUS: CALCIUM APPEARS TO INHIBIT LICAND BINDING
RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT
CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR.
SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                      AND HEAR DOMAIN:
                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM SHORT FORM/TIPR; ARE PRODUCED BY ALTERNATIVE STISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND
                                                                                                                                                                                                                                                                                                                                                                                                      reticulum.
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                                                                                              D26350; BAA05384.1;
                                                                   HGNC: 6181;
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               IPR000699; Ca-rel_channel.
IPR001682; Ca/Na_pore.
IPR000493; InsP3_receptor.
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Furuichi
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RESULT 12
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Best Local :
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15-JUL-1998
15-JUL-1998
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SMART; SM00472; MIR;
         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                              Caenorhabditis elegans
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                                                                                                       CAEEL
                                                                                                                                                           RYFKGDYSIGV-----NG--HLSGAYSKTAQVGGSFSGQDSD 1736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Transmembrane; Glycoprotein; Phosphorylation;

Transport; Calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2701
                                                            (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation updat
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                                                                                                       STANDARD;
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                    Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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            Caenorhabditis
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POTENTIAL.
EXTRACELLULAR
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IVVGDK -> DASFWI (IN SHORT
MISSING (IN SHORT ISOFORM)
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RESULT 13
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Matches 61
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Chissoe S., Hawkins J.;
Chissoe S., Hawki
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
16-OCT-2001
SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
Gregor J., Davis N.W., Kirkpatrick H.A., Go
Mau B., Shao Y.;
"The complete genome sequence of Escherichia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  Hypothetical o
                                                                                                                                                                                                                                                                                                                                                                                                                                              P45420;
                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                           Escherichia coli
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EQUENCE 525 AA;
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InterPro; IPR001575; Oxid_
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
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_binding_4; 1.
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  sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                       gamma subdivision; Enterobacteriaceae;
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Pred. No. 16;
50; Mismatches
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protein yho
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                                           .A., Perna N.T., I
., Rode C.K., Mayl
, Goeden M.A., Ro
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                                                                                                                                                                                                                                                                                                                                            precursor
                                                                 K., Mayhew
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                                                                      Burland V.,
/hew G.F.,
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COPP YEAST STANDARD; PRT; 889 AA.
P41811;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
SEQUENCE
                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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PROSITE; PS01151; FIMBRIAL USHER; 1.
Hypothetical protein; Outer membrane
SEQUENCE FROM N.A.,
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-!- FUNCTION: INVOLVED IN T
                                            NCBI_TaxID=4932;
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SEQUENCE OF
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Pred. No. 30;
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PRODOM; PD000018; WD40; 3.
SMART; SM00320; WD40; 6.
SMART; SM00320; WD REPEATS 1; 1.
PROSITE; PS50082; WD REPEATS REGION;
PROSITE; PS50294; WD REPEATS REGION;
PROSITE; PS50294; WD REPEATS REGION;
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or send a
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MEDLINE=96437978; PubMed=8840506;
BESCRIDANO V., Eraso P., Portillo F., Mazon M.J.;
Escribano V., Eraso P., Portillo F., Mazon M.J.;
"Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces
cerevisiae chromosome VII reveals SEC27, SSM1b, a putative
S-adenosylmethionine-dependent enzyme and six new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95014199; PubMed=7929113;
Duden R., Hosobuchi M., Hamamoto S., Winey M., Byers B., Schekman "Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits essential for endoplasmic reticulum-to-Golgi protein traffic.";
J. Biol. Chem. 269:24486-24495(1994).
                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                   EMBL; U11237; AAA61711.1; -.
EMBL; X92670; CAA63359.1; -.
EMBL; Z72659; CAA96848.1; -.
SGD; S0003105; SEC27.
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Harter C., Draken E., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 12:887-892(1996).
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                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR001680; WD40
19 WNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQ-SLPDVFSTDSIFLPYLVS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NETWORK: COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI MEMBERANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER TRANSPORT OF DILYSINE-TAGGED PROTEINS.
SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
BUTA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (S an email to license@isb-sib.ch).
                                                 Similarity
                                                                                                            332:71-73 (1993)
                                                                                                                                                                                                                            Protein
                                  Conservative
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41
83
15
125
169
214
256
99444 MW;
                                               5.4%;
19.8%;
                                  58;
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                                               Score
Pred.
                                                                                                                                                                                                                       Golgi
                                                                                               6ASES0BBEB02CB58 CRC64;
                               ed. No. 36;
Mismatches
                                               No.
                                                                                                                                                                                                                         stack; Membrane; Repeat;
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                                                              .
5-
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                                                              DB 1;
                                127;
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P75056;
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SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
MEDLINE=07105885, Hilbert H., Plagens
                                                 LIPID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                     InterPro; IPR000044; Lipoprt_MG045.
Pfam; PF02030; Lipoprotein_8; 1.
PRINTS; PR00905; MYCMG045.
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Nucleic Acids Res.
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16-OCT-2001
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                                                                                                                                                                                                                             modified and this statement is not remov
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                                                                                                             Hypothetical protein; Lipoprotein;
                                                                                                                           PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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 61;
              Similarity
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                                                  55019
             5.3%;
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Score 96; DB
Pred. No. 16;
17; Mismatches
                                                 HYPOTHETICAL LIPOPROTEIN MG045
N-ACYL DIGLYCERIDE (POTENTIAL)
; 1AD4E0AB211B64F8 CRC64;
                                                                                        POTENTIAL
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24 NEVKLINLIKDVLPTQVSGYNIEY--TEFDCYSDASLQ--SLPDVF--STDSIFLPYLVS

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A; Residues: 1-409 < C
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Result

	98	98.5	98.5	98.5	99	99	99	99	99	99.5	100	100	100.5	100.5	101
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N	N	N	N	N	N	N	2	N	N	N	N	N	N	N	2
A81315	H90083	A90428	E86626	I40589	T25421	S22768	T45691	F70028	833921	S62460	D81746	S77508	B86210	E64559	H70203
probable MCP-type	polyadenylate-bind	serine proteinase,	transcription-repa	parasporal crystal	hypothetical prote	130K protein - mai	receptor-like prot	transmembrane rece	alpha-amylase (EC	hypothetical prote	type III secretion	srrA protein - Syn	protein F22G5.6 [i	outer membrane pro	isoleucine-tRNA li

ALIGNMENTS

C;Keywords: transferase C;Keywords: transferase F;1-30/Domain: signal sequence #status predicted <SIG> F;31-409/Product: thiamin pyridinylase #status predict A;Cross-references: EMBL:U17168; NID:g984284; A;Experimental source: strain 168 C;Complex: monomer [validated, MUID:96216437] J. Biol. Chem. 271, 3445-3452, 1996
A;Title: Mechanistic studies on thiaminase I: overexpression A;Reference number: 224363; MUID:96216437; PMID:8631946
A;Accession: T47118 thiamine pyridinylase (EC 2.5.1.2) precursor [validated] - Paenibacillus thiaminolyticu: N;Alternate names: pyrimidine transferase; thiaminase I C;Species: Paenibacillus thiaminolyticus C;Species: Paenibacillus thiaminolyticus C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Jun-2002 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Jun-2002 C; Accession: T47118 R; Costello, C.A.; Kelleher, N.L.; A;Description: EC 2.5.1.2 [validated, MUID:96216437] A;Status: preliminary; translated from GB/EMBL/DDBJ Query Match
Best Local Similarity
Matches 90; Conserv 278 AVEVIKNILITNTLVLDLLGLGL------TLPANKNGIAHLAKSSNFYAQLSQ 323 LLSSPNGTQ--QASSLLELAQKVG---YEQIYYPD-----VASSSSFTVFGLYQQLLQSS 171 LDSIFLSHFVDAGYLLPFGSQDIDQA-----EDVLPFALQGAKRNGEVYGLPQILCTNL 146 TLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFS --ELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYSELAQ 368 --ALIDVTGQYTEYDLLPPLDPLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWFA SSAAVDIKAS----DLPQSGDQVNKDITQKYRTILDST-----VVASQREYINSVKQG LFYRKGDLKIGOVDNIYELYKKIGTSHSEQIPPPONKGLLINMAGGTTKASMYLE----TDSIFLPYLVSLG-----GVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNF 121 KPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTS---DKPYVYTDVLALNSNLCDEKQKV 277 TLKVAIYPYVP-----DPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDL-DVFV 92 1-409 <COS> Conservative 12.8%; Score 230; DE 25.2%; Pred. No. 1.1e cive 53; Mismatches Abe, M.; McLafferty, F.W.; Begley, DB 2; ..1e-08; PIDN:AAC44156.1; PID:g833806 predicted <MAT> 146; Length 409; Indels and identification of 68; T.P. Gaps 259 220 201 99 14; the

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hypothetical protein T8K14.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96827
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chin, S.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Anuthors: Salzberg, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96827
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B96827
                                                                                                                                            phycobilisome linker protein apcE - red alga (Porphyra purpurea) chloroplast C;Species: chloroplast Porphyra purpurea C;Cate: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 10-Sep-1997 C;Accession: S73184 R;Reith, M.; Munholland, J. Plant Mol. Biol. Rep. 13, 333-335, 1995 Plant Mol. Biol. Rep. 13, 333-335, 1995 Plant Mol. Biol. Rep. 13, 333-35, 1995 Plant Mol. Biol. Rep. 13, 335-35, 1995 Plant Mol. Biol. Plant Mol. Biol.
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A<sub>f</sub>Molecule type: DNA
                                     A;Accession: S73184
A;Status: preliminary;
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Best Local S
Matches 75
                                                                                                                   ;Reference number: S73108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 LONMLEEYNEMENRGGSOKLRMFLFS--ISDMDDALLGVNKNDGDSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LELAQKVGYEQI------VYPDVASSSSFTVFGLYQ-----QLLQSSSSAAVDIKASD-
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A;Residues: 1-886 <REI>A;Cross-references: EMBL.
A;Note: the nucleotide ss
C;Genetics:
A;Gene: apcE
A;Gene: chloroplast
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                       R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redcarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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A; Residues: 1-613 < KUR>
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                                                                                                                                                                                                                                                                                                                  A; Reference number: A99139
A; Accession: B90294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SSO1375 [imported] - Sulfolobus solfataricus
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                                                                                                                                                                                                                                                A;Cross-references: GB:AE006641; NID:g13814587;
                                                                                                                                                                                                                                                                                                                                                      A; Description: Sulfolobus
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Best Local :
                                                                                                                                                                                                                               Genetics:
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Best Local :
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                                                                                                 13 FPY---LPSWNENG------NEVKLINL-IKDVLPTQVSGYN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDASLQSLPDVFSTDSIFLPYLVSLG-GVKSLDESLVRGVTGDL------HSFVS--SS 103
ATYKNIAIIIISYKDĖSKY-NITLSQYPSHILQGTDGIGL-FIIPLQALPWVYGKSVNSS
                                -----IEYTEFDCYSDASLQSLPD--VFSTDSIFLPYLVSLGGV-----KSLDES
                                                                   YPYNQVMFNYPENGPLELNMSYDNWSIHEISFIALPTVDVYPTKI--YNSSLYLGKGLLS
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                                                                                                                                                           19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%; Score 115.5;
20.5%; Pred. No. 4.3;
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                                                                                                                                           72;
                                                                                                                                         Score 111.5;
Pred. No. 4.7;
72; Mismatches
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A;Cross-references: EMBL:Z68198; PIDN:CAA92385.1; GA;Experimental source: strain 972h-; cosmid c18G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCN1 homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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A;Accession: T37919
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                                                                                                                                                                                                                                                                                                                                                                     1492
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                        EILKNTSSPVPHIRESFISLLIYLPATFGSRFQPYLARAIPPILSGLADDSELVQTASLR 178:
                                                                                                                                                                                           PILKYGLRERNAGTKROSAKIFGLMASLTEPENLAVYLESLMPRLREVLIDPVPDTRATA 166:
                                                                                                                                                                                                                                                                                ANKSLLRFGDVISNPEIQTLVPTLLKALSDCTRYTDDALEALLKTSFVHYLDPPSLALVI 160:
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                                                                                                                                                 LPQSGDQVNKDITQKYRTILDS--TVVASQREYINSVKQGKPISNYYVGYSESMCE--IK 238
                                                                                                                                                                                                                                                                                                                                                                   EYNWRSKKASVEILGLMSYMAPKQLSVFLPTI----IPKLSEVLT-----DSHSQVRNT 1541
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                                                                                                                                                                                                                                    -ASSSSTTVFGLYQQLLQSSSSAAV------DIKASD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 111.5;
19.7%; Pred. No. 45;
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                                                              ----YNVQLIGTSDKPYVYTDVLALNSNLCDEK----OKVAVE 280
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                                                                                           R.Du, Z.; Le, T.T.
R.Du, Z.; Le, T.T.
submitted to the EMBL Data Library, Decemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fimbrin/plastin-like protein - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #tex
C;Accession: T06799
R;Cruz-Ortega, R.; Cushman, J.C.; Ownby, J.D.
Plant Physiol. 114, 1453-1460, 1997
A;Title: cDNA clones encoding 1,3-beta-glucanase and a A;Reference number: Z15824; MUID:97422889; PMID:9276954
A;Accession: T06799
A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-998 <DUZ>
                                                            A;Description: The sequence A;Reference number: Z21225 A;Accession: T32787
                                                                                                                                                                   hypothetical protein F14D2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C;Accession: T32787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U67717; NID:g1575594; PIDN:AAC49813.1; PID:g1575595
A;Experimental source: cv. Victory; root; 4 days old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-448 <CRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description: actin-bundling;
Superfamily: plastin; alpha-actinin actin-binding domain homology;
Keywords: actin binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                 341 ---LNWANSKVK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 LYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQK---YRTILDSTVVASQREYINSVKQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 AYAYLLKALAPE-TSPETTLETKNPDERAKMVLEQAEKLDCKRYLTPKDITEGSANLNLA 177
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                                                                                                                                                                                                                                                                                                                                                                                       LRCVDFANKEVK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKFSLVNLAGNDIVQGNKKLIVALLWQLMRFNILQLLNRLRSHSKGSQGKQITDADI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EV---IKNLLTNTLVL--DLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DVRNGWV-----LLEVLDKVSPGSVNWKL---ESKPPIKLPFRKLEN--CNQVVKIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVAQIFQHRNGLTSDIKQVTLTQSASRDDVLVSREERAFRMWINSLGVES---YLNNVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPOLVELFDDSKDIDEVLSL----STEKMLLRWMNHHLKKAGYKKTVNNF--SSDVKDGE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPDVFS--TDSIFLPYLVSLGGVKSLDESLVR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNPWERNENHTLCLNSAKAIGCTVVNIGTQFLVEGRPHLVLGLISQIIKIQLLADLNLKK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPSWNENGNEVKLINLIKDV-------LPTQVSGYNIEYTEFDCYSDASLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAKMI VNNYATKSVDLL----LPELEKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 2;
Pred. No. 4.4;
2; Mismatches 155
                                          from GB/EMBL/DDBJ
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A;Experimental source: strain Bristol N2; clone F14D2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F53F4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jan-2000
C;Accession: T22583
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                          ;Map position: 5
;Introns: 47/3; 110/3; 151/1; 198/3; 352/3
;Superfamily: dimethylaniline monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Reference number:
;Accession: T22583
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                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP:F53F4.5
                                                                                                                                                                                                                                                                                                                                                                                                                        Folecule type: DNA
idues: 1-528 <WIL>
Ser-references: EMBB: Z77663; PIDN:CAB01214.1; GSPDB:GN00023; CESP:F53F4.5
Experimental source: clone F53F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                             ALANLLCAGYITITEDIDTFTENSVIVKGGREFKCDIFLTCTGYTFGFP
                                                                                                                      SLDESLVRG----VTGDLHSFVSSSASVNGS-----
                                                                                                                                                          YDVQL--FSRYYDTLLKTIPHAVAND--FMEYRLQQRMDHDVYGLRPDHRFFQQHPTVND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QREYINSVKQGKPISNY-YVGYSESMCEIKD-----IIRDQQ----YNVQLIGTSDKPY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOSSSSAAVDIKASDLPQSGDQVNKDITQK----
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                                   PNGTQQASSLLELA-QKVGYEQIVYPDVASSSSFTVFGLYQQL-----LQSSSSAAV 176
                                                                                                                                                                                                  YNIEYTEFDCYSDASLOSLPDVFSTDSIFLPYLV-----SLGGVK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQVFARTNLKIYGFEV----QICKDLFRKDGQKTCIFKDLSMLDPKCQHIIGDIFINAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 6.0%; Score 108.5; Similarity 22.6%; Pred. No. 16; 76; Conservative 56; Mismatches
                                                                                                                                                                                                                                           Similarity 59; Conserv
-DSDIVEIKNQQVPLYKYVFP--PNSDSVAVIGLIQPIGSIAPISEIQSRWAARV
                                                                                                                                                                                                                                       6.0%; Score 108; DB llarity 21.7%; Pred. No. 6.6; Conservative 47; Mismatches
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                                                                                                                                                                                                                                                                               2; Length 528
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                                                                                                                    ----VYGFPQYLCSNFLLSS 125
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R;Apt, K.E.; Grossman, A.R. submitted to the EMBL Data Library, A;Description: Characterization and
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A; Residues: 1-885 < APT >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phycobilisome anchor protein apcE - red alga (Aglaothamnion neglectum) C;Species: chloroplast Aglaothamnion neglectum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 06-Feb-C;Accession: S20621; S61554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 YSDASLQSLPDVFS-TDSIFLP-----YLVSLGGVKSLDESLVRGVTGDLHSFVSS--S 103
                                                                              QQFDAKESEVRV
                                                                                                              LASQGLSSFIT---VLVNSNEYNQVFGVNIVPYRRFTTLPA----ANFPNTEKLYNTLT
                                                                                                                                              VAVEVIKNLLTNTLVL---
                                                                                                                                                                             LVNNNITVQQF-IEQIGSSSLYGREFYQPYPNTKVIELGTKHFLGRAPNNQAEIRYYNQI
                                                                                                                                                                                                                                                                         NKDITQKYRTILDS----TVVASQ---REYINSVKQ---GKPISNYYVGYSESMCE--
                                                                                                                                                                                                                                                                                                           YIRSFGDNTVPYERYITSANMILKSNYSNFLYSTLKTKNSNSKKFIELSNILEKRSLNSI 696
                                                                                                                                                                                                                                                                                                                                          SFTVFG---
                                                                                                                                                                                                                                                                                                                                                                         SSVFRSLYWEPLYICKAIEYIHYRLLGRPSYGRQEINQYFDIVYREGYYKMIDYLLNSSE 636
                                                                                                                                                                                                                                                                                                                                                                                                       ASVNGSVYGFPQYLCSNF-----LLSSPN-GTQQASSLLELAQKVGYEQIVYPDVASSS 156
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                                                                                                                                                                                                                                         QARISQGVSTVRDQYKVFQLTQLSSQVDKRQVVKAIYRQIFERDLNSFAIGDEFINLEKA
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                                              KQ----SSEIIV
                                                                                                                                                                                                           -IKDIIRDQQYNVQLIGTSD------KPYVYTDVLALN-----SNLCDEK---QK 276
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                                                875
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                                                                                                                                              -DLLGLGL----
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d transcript
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C;Accession: A96714
R;Theologis, A.; Ecker, J.R.; Palm, C.
Chin, C.W.; Chung, M.K.; Conn, L.; Co
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,

C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

#text_change 31-Mar-2001

Johnson-Hopson, C.; Khan, S.; S.X.; Liu, Z.A.; Luros, J.S.;

Khaykin, E.; Kim, C Maiti, R.; Marziali A96714
hypothetical protein T6L1.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change

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A; Nolecule type: DNA
A; Residues: 1-2819 <KUR>
A; Cross-references: GB: AL445566; PID: g14089727;
A; Cross-references: strain UAB CTIP
                                                                                                                                                                                             R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: A99551
                                                                                                                                                                                                                                                                                                                                                                 RESULT
A90551
                                                                                                                                                                                                                                                                                                       conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (C;Species: Mycoplasma pulmonis (C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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A; Residues: 1-1033 <STO>
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A;Authors: Salzberg, S.L.; Schwarcz, J.R.; Shinn, P.; Southwick, A.M.; Sun,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96714
                                                                                                                                                                                 A; Status: preliminary
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 Query
Best L
                                                      :Genetic code:
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 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LMLVTAKYNRELDSFASETSDQILRNLEKCPENIKOMAESGLLEPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSNFYAQLSQQFD--AKESEVRVLRCVDFANKEVKNCA--GVLRPFL
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Pred. No. 24;
Score
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106
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1.1e+02;
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                                                                                                                            PIDN:CAC13486.1; GSPDB:GN00153
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <KAM>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49115.1; PID:g54576.
                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July A;Description: Pyrococcus abyssi genome A;Reference number: A75001 A;Accession: D75208
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                                                                                                                                                                 19 WNENGNEVKLINLIKDVLPTOVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSL
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IRKDVAKCVGLDVSTLPDKVKNGEFTWSDVYE
                                ---ELAQKVGYEQIVYPDVASSSSTVFGLYQ 165
                                                                 GYILDITDYAKAYQSVLNDFYPSLLEAAKYKGRLYGLPQ-
                                                                                                  GGVKSLDE--SLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLL 136
                                                                                                                                WKENGINVKIV-IPEDMIRYDOS-FKDQYQEF--LSKQPLGQAGDFFVNSYAFLPNLAEE 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKNKYLAYENLNDFLIDALVDNKENIINLSSNTLGKIKTDDEFKNIIKSFITKNLMTSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENITHKALDQQNSY--FAVIKTLL-----SVKEGDVDKSDE--FKAIIKKFLNLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQIVYPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGY 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRCVDFANKEV
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                                                                                                                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                 Score 106;
Pred. No. 9.
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G82934
hypothetical protein UU094 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change C;Accession: G82934

#text_change

20-Aug-2000

RESULT

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A;Residues: 1-1054 <GLA>
A;Cross-references: GB:AE002109; GB:AF222894; NID:g6899045; PIDN:AAF30500.1; GSPDB:GN00:A;Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, A; Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, Jok, C.; Schlueter, T.; Simoes of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1746
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A;Molecule type: DNA
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A;Residues: 1-358 <GLA>
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Best Local
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20.9%; Pred. No. 5.5;
tive 44; Mismatches
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Fsihi, H.
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
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A;Cross-references: GB:AE000785; NID:g2689951; PIDN:AAC66031.1; PID:g2689960; TIGR:BBB0
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein BBE02 - Lyme disease spirochete plasmid E/lp25
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
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                                      VLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQF----DAKES 330
                                                                             SIIEFKD---NEEFT--LINK----MFSKFSALGEGYIDFKKGLDPSIKNRKSLLKE--
                                                                                                               SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKV--AVEVIKNLLTNTL
                                                                                                                                                        S----FKAKFMIQSSDNILKEITRDLKDSKDDAYKGIELN-INQIKKLSPI-----QE
                                                                                                                                                                                         SAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSE
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                                                                                                                                                                                                                                                                                                               -----DPNLFRYFVTF-NLKLIKEK-----GNL-TYLVPSAIWNESSSRILRKHI 883
                                                                                                                                                                                                                                                                                                                                                       QSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGS-----VYG
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22.1%;
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Search completed: January Job time : 28 secs

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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sult No.	Score		Query Query Match Length	DB	ID	Description
μ	100.5		745	œ	US-08-834-666A-6	Sequence 6, Appli
N	97.5		2037	9	US-09-951-402-3	Sequence 3, Appli
w	97.5		2037	10	US-09-951-401-3	Sequence 3, Appli
.4	97.5		2037	10	US-09-922-101-3	Sequence 3, Appli
ຫ	97		615	9	US-09-992-598-194	Sequence 194, App
σ	97		615	9	US-09-989-293A-194	Sequence 194, App
7	97		615	9	US-09-989-735-194	Sequence 194, App
æ	97		615	9	US-09-990-444-194	Sequence 194, App
ø	97		615	9	US-09-989-730-194	Sequence 194, App
10	97		615	v	US-09-990-436-194	19
H	970		615	9	US-09-991-181-194	19
12	97		615	9	US-09-993-687-194	19
13	97	5.4	615	9	US-09-989-734-194	Sequence 194, App
14	97		615	9	US-09-997-653-194	19
15	97		615	10	US-09-989-722-194	e 1
16	97		615	10	US-09-989-723-194	_
17	97	5.4	615	10	US-09-989-279-194	<u>, .</u>
18	97	5.4	615	10	US-09-989-727-194	щ.
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                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-951-402-3
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 2037
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                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/951,402
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
PRIOR FILING DATE: 1999-05-07
RIOR APPLICATION NUMBER: US 60/084,740
NOR FILING DATE: 1998-05-08
UMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting
FILE REFERENCE: MMSC2
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 SGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYY-VGYSESMCEIKDIIRDQ 244
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                                                                                                                                                 778 TVRIGVAKPLPLSPEEG----YVSAKED-----SFLYPPHSC-EEAGLADKP-LFR 822
                                   127 NGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLY------QQLLQSSSSAAVDI 178
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                                                                                                                                                                                                                           Local Similarity 21.4 res 75; Conservative
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 DGLNYGSSLPSSPPK---
                                                                                                          TDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSP 126
                                                                                                                                                                                    TLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYNVQLIGTSDKPYVYTDVLALNSNLCDE-----KQKVAVEVIKNLL-----
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internal
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21.4%; Pred. No. 11;
ative 48; Mismatches 147;
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--DVIENSCDPVLDLHMSLEELYTQNLLQRQDENTPSV 919
                                                                       TFESPYSPENDSIYSTQASILSLHGSSCG
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CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 09/306,998
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 60/084,740
PRIOR FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
TYPE: PRT
ORGANISM: Homo sapiens
US-09-951-401-3
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US-09-922-101-3
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Matches
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CURRENT FILING DATE: 2001-09-14
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APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- An MMAC1 Interacting
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                                                                                    1015 NSSLGMTVSANKDGLGMIVRSIIHGGAIS-----RDGRIAIGDCILSINEE
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Local Similarity 21.4%; Pred. No. 11;
hes 75; Conservative 48; Mismatches 147;
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Sequence 3, Application US/09922101 Patent No. US20020146711A1 GENERAL INFORMATION:

APPLICANT: Bartel, Paul L. APPLICANT: Tavtigian, Sean V. TITLE OF INVENTION: MMSC2- An

MMAC1 Interacting Protein

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-922-101-3
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/306,998
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
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PLICANT: Baker, Kevin P.
PLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                    INVENTION:
     INVENTION:
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Godowski, Paul J
Grimaldi, J. Christopher
                                               Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                    Tumas,
                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                              Napier, Mary A.
                                                                                                                                                                                                 Gurney, Austin L
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
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                                                                                                                                                Nicholas F.
                                   Zemin
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Secreted and Transmembrane Polypeptides Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088655
OR APPLICATION NUMBER: 60/088734
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OR FILING DATE: 1998-06-10
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OR FILING DATE: 1998-06-10
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OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
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OR APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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FILING DATE: 1997-06-16
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FILING DATE: 1998-06-05
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60/089512 60/089440

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OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/09163
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/09163
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                                                   Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                       Ashkenazi, Avi J
Baker, Kevin P.
                                                                                                                                             Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                     Eaton, Dan
                                                                                                                                                                                                                                                      Botstein, David
   Paoni, Nicholas
                                   Napier, Mary
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Pred. No. 2.3;
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APPLICATION NUMBER: FILING DATE: 1998-0

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60/090690 60/090678 60/090676 60/090557 60/090542 60/090540 60/090535 60/090472 60/090445 60/090444

APPLICATION NUMBER: FILING DATE: 1998-0

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APPLICATION NUMBER: 60/090246

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1998-06-19 1998-06-19 1998-06-18

60/089952 60/089948 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0

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CURRENT APPLICATION NUMBER: US/09/989,293A

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APPLICATION NUMBER: 60/088738
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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APPLICATION NUMBER: 60/088876
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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PRIOR FILING DATE: 1997-10-17
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
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DR FILLING DATE: 1998-06-03
DR APPLICATION NUMBER: 60/088021
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DR APPLICATION NUMBER: 60/088025
DR FILLING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/084600
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Kljavin, Ivar J.
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OR APPLICATION NUMBER: 60/090535

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APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
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RESULT 8
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; Sequence 194, Application US/09990444
; Publication No. US20020193300A1

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CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065316
PRIOR PRILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PRILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILLING DATE: 1998-02-25
PRIOR PRILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/08910
PRIOR PRILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILLING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/087827
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Grimaldi, J. Christopher
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Goddard, Audrey
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Eaton, Dan L.
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Botstein, David
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, Margaret Ann
wart, Timothy A
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/091519
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APPLICATION UNMBER: 60/090695
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                                                    NUMBER: 60/091978
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
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Tumas, D
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Williams, P. Mickey
Wood, William I.
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Godowski, Paul J.
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Gerritsen, Mary E.
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art, Timothy A.
                                                 NUMBER: 60/087609
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Query Match 5.4%; Score 97; DB 9; Length 615; Best Local Similarity 21.3%; Pred. No. 2.3;
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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FILE REFERENCE: P2730P1C11
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Roy, Margaret Ann
Stewart, Timothy A
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Tumas, Da
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Kljavin, Ivar J.
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Godowski, Paul
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087609 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910 FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06 APPLICATION NUMBER: LING DATE: 1998-03-NUMBER: 60/089440 1998-06-16 1998-06-12 1998-06-11 1998-06-09 1998-06-16 60/089514 60/089512 60/089105

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OR APPLICATION NUMBER: 60/091633
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OR APPLICATION NUMBER: 60/091978
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OR APPLICATION NUMBER: 60/091982
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OR APPLICATION NUMBER: 60/092182
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                                                                                                   Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Grimaldi, J. Christopher
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Kljavin, Ivar J.
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CURRENT APPLICATION NUMBER: US/09/989,734
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/091360
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                                                     Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
                                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E.
                                           Pan, James
                                                                                                                                                                                                                Fong, Sherman
                                                                                                                                                                                                                                  Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                                                                                                                                                        Desnoyers, Luc
                     Paoni
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b. US20030008297A1
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i,Nicholas F.
Margaret Ann
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Pred. No. 2.3;
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OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/049787
OR FILING DATE: 1997-06-16
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DR APPLICATION NUMBER: 60/088734
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-06-02
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Williams,
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P. Mickey
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OR APPLICATION NUMBER: 60/090696
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OR APPLICATION NUMBER: 60/090863
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OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091360
OR APPLICATION NUMBER: 60/091360
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OR FILING DATE: 1998-07-02
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DR FILING DATE: 1998-07-02
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DR APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090678
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                 Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
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                                                                                                   Baker, Kevin P. Botstein, David
Gerritsen, Mary
                                                                                 Desnoyers, Luc
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CURRENT APPLICATION NUMBER: US/09/989,722
ENTRENT FILING DATE: 2001-11-19
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Godowski, Paul J.
Grimaldi, J.Christopher
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Kljavin, Ivar :
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art, Timothy A.
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OR APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/091544
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rived by analysis of the total score distribution.
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al Similarity 20.5%; Score 139.5; DB 4; Length 10182; al Similarity 20.5%; Pred. No. 0.0095; B9; Conservative 59; Mismatches 140; Indels 147; G NEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSLGGVKS	ESULT 1 S-09-134-001C-3159 Sequence 3159, Application US/ Patent No. 6380370 GENERAL INFORMATION: NUCLEIC A TITLE OF INVENTION: NUCLEIC A TITLE OF INVENTION: EPIDERMI FILE REFERENCE: GTC-007 CURRENT FILING DATE: 1998-08 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 3159 LENGTH: 10182 TYPE: PRT ORGANISM: Staphylococcus epi ORGANISM: Staphylococcus epi	**************************************
77.7%; Sco ilarity 20.5%; Pre CONSERVATIVE 59; NLIKDVLPTQVSGYNIEYTEF	Pation 1 Pette-S: NUCLEIC EPIDE: 007 1998 NUBER: 1998-11 MBER: 1997-11 MBER: 1997-88 1997-08 1997-08	2236667 2336667 210988 2110988 2110988
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                                    Sequence 2, Application US/07915203
Patent No. 5359048
GENERAL INFORMATION:
APPLICANT: Ohba, Michio
APPLICANT: Iwahana, Hidenori
                                                                                                                     Sequence
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LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/134,001C
URRENT FILING DATE: 1998-08-13
LIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                Iwahana, Hidenori
Sato, Reiichi
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Best Local Similarity 22.6%;
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
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TITLE OF IN
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FILING DATE: 19920723
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1ii
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1046 VQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVT--ARKE 1085
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                                                                  IPGMNYTSFTE
                                                                                                    --ALNSNLCDEKQKVAVEVIKNLLTNTL--VLDLLGLGLTLPAN--KNGIAHLAKSS---
                                                                                                                                      KTYY-AAKQA--IDRLFADYQDQKLNSGVEMSDLLAAQNL-VQSI-----PYVYNDALPE
                                                                                                                                                                    REYINSVKQGKPISNYYVGYSE----SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVL--
                                                                                                                                                                                                        TTNGNATLGNL -- EFVEEG ----
                                                                                                                                                                                                                                                                           CGGVDRCSEQQYVDANLALENNGENGNMSSDSHAFSFHIDTGEIDLNENTGI-WIVFKIP 900
                                                                                                                                                                                                                                                                                                                                                 ----YQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVRPVNS
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                                                                                                                                                                                                                                         ASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVN--KDITQKYRTILDSTVVASQ 210
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VENTION: No. 5359048el Microorganism and Insecticide
EQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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Sakanaka, Kazunobu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                              NFYAQLSQQFDAKESEVRVLRCVDFANKE 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98.5; DB
Pred. No. 2.3;
58; Mismatches
                                                                  LTNRLQQAWNLYDLQNAIPNGDFRNGLSNWNATSDVN 1045
                                                                                                                                                                                                        -----PLSGETLEWAQQQEQQWQDKMARKRAASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126;
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                                                                                                                                                                                                                                                                                                                                                                                   -NGSVYGFP-----
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RESULT 4 US-08-272-887-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 1149 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                       ry Match
5.5%; Score 98.5;
L Local Similarity 22.6%; Pred. No. 2.
ches 91; Conservative 58; Mismatche
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TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
NIMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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ZIP: 32606
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  265
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                                                                           211 REYINSVKQGKPISNYYVGYSE----SMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVL--
                                                                                                                                                        153 ASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVN--KDITQKYRTILDSTVVASQ 210
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CITY: Gainesville
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REGISTRATION NUMBER: 31,79
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--ALNSNLCDEKQKVAVEVIKNLLTNTL--VLDLLGLGLTLPAN--KNGIAHLAKSS---
                                                                                                                                                                                               CGGVDRCSEQQYVDANLALENNGENGNMSSDSHAFSFHIDTGEIDLNENTGI-WIVFKIP 900
                                                                                                                                                                                                                                                                                                                    SLGGVKSLDESLVRGVTG-DLHSFVSSSASV-----NGSVYGFP------
                                   KTYY-AAKQA--IDRLFADYQDQKLNSGVEMSDLLAAQNL-VQSI-----PYVYNDALPE
                                                                                                                  TTNGNATLGNL--EFVEEG------PLSGETLEWAQQQEQQWQDKMARKRAASE 946
                                                                                                                                                                                                                                     ------QYLCSNFLL--SSPNGTQQASS-----LLELAQKVGYEQIVYPDV 152
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GY: linear
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2421 N.W. 41st Street, Suite A-1
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Sakanaka, Kazunobu
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Mismatches 126; Indels 127;
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Parent No. 5824878
                                                                                                                                                                           Matches
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/272,887
FILING DATE: 08-JUL-1994
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 1149 amino aci
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 904-375-8100
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                                786 ----YQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVRPVNS
                                                                   77
                                                                                                                                     26 VKLINLIKDVLPTQVSGYN-----IEYTEFD-CYSDASLQSLPDVFSTDSIFLP-YLV 76
                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                   SLGGVKSLDESLVRGVTG-DLHSFVSSSASV-----
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FL
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Vawasuqi, Tadaaki
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Sato, Reiichi
                                                                                                                                                                          Conservative
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--- QYLCSNFLL--SSPNGTQQASS----
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                                                                                                                                                                          58;
                                                                                                                                                                        Score 98.5; DB 2;
Pred. No. 2.3;
B; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version
---LLELAQKVGYEQIVYPDV 152
                                                                   -NGSVYGFP----- 114
                                                                                                                                                                                                         Length 1149;
                                                                                                                                                                          Indels 127;
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RESULT 7
US-09-134-001C-5661
S-09-134-001C-5661, Application US/09134001C
; Patent No. 6380370
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Best Local Similarity
Matches 67; Conserva
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACTYER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-336-447A-7
GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09336447A Patent No. 6310190
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APPLICANT: EREDENBURG, ROSS A.
APPLICANT: EREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:0.24
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                        KOKVA-----VEVIKNLLTNTLVLDLLGLGLTLPAN-KNGIAHLAKSSNFYAQLSQQFDA 327
                                                                                                                                                                                                                                                                                                                                                                               STDAVNGSQLY-----ALATAVDDNQYDIEINQDNI-KDL-QKEVKGLDKEVGVLSRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRARVNG-----LTLKNFSGVSKADNGTVSVGS-----QGKERQIVHVGAGQISDD
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    INFORMATION
                                                                                                                                      HSSDIKTLAKASAANTDRIAKNKA 448
                                                                                                                                                                              KESEVRVLRCVDFANKE--VKNCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                    SSFTVFG--LYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREY 213
                                                                                                                                                                                                                   QADIAKNQADIKTLENNVEEGL-LDLSGRLIDQKADIDNNINHI----
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US-09-540-824-26
; Sequence 26, Application US/09540824
; Patent No. 6383753
; GENERAL INFORMATION:
; APPLICANT: Thiele, Dennis
; APPLICANT: Liu, Phillip
; APPLICANT: Liu, Phillip
; TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Prolifera
                                                                                                                                                                                  ; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-540-824-26
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SEQ ID NO 5661
LENGTH: 639
TYPE: PRT
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                          Matches
                                                                                                                                                                                                                                                                                                     FILE REFERENCE: UM-04266
CURRENT APPLICATION NUMBER: US/09/540,824
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                           24 NEVKLINLIKDV----LPTQVSGY-NIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSL
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SHVEFVQLLKGLDYKDYPTVVSRIRTLHHVKLHPDNKSRLEN----FSV--ILLQHILHL
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22.5%; Pred. No. 1.1;
ative 59; Mismatches
                                                                                     5.4%; Score 97.5; I
19.7%; Pred. No. 1.7;
tive 65; Mismatches
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                                                                                          Indels 135;
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US-09-306-998-3
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SEQ ID NO 3
LENGTH: 2037
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 5.4%; Score 97.5; DB 4; Length 2037; Best Local Similarity 21.4%; Pred. No. 7.2; Ches 75; Conservative 48; Mismatches 147; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09306998 Patent No. 6291173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bartel, Paul L.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: MMSC2- AN MMAC1 Interacting
FILE REFERENCE: MMSC2
CURRENT APPLICATION NUMBER: US/09/306,998
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 60/084,740
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEO ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
     1015
                                          294 LIGIGITLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANKE 344
                                                                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                                                                                                          823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVRIGVAKPLPLSPEEG----YVSAKED-----SFLYPPHSC-EEAGLADKP-LFR 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVCKKLYIANLELKEQSYSHRYVPEVITAVSQALYLLYPNFISIVPGTFALPDSLKE--- 624
NSSLGMTVSANKDGLGMIVRSIIHGGAIS-----RDGRIAIGDCILSINEE 1060
                                                                                          SAELPSVLPDS-----AGKGSEYLLEQSSLACNAE-CVMLQNVSKESFER--TINIAKG 1014
                                                                                                                                       MCBIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLD 293
                                                                                                                                                                                      DISMGPASGFTINDYTPANAIEQQYE--CENTIVWTESHLPSEV-----IS
                                                                                                                                                                                                                                                                                          DGLNYGSSLPSSPPK--
                                                                                                                                                                                                                                                                                                                                                                                  ADLA----LVGTNDADLVDES-----TFESPYSPENDSIYSTQASILSLHGSSCG 868
                                                                                                                                                                                                                                                                                                                                                                                                                               TDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSP 126
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                                                                                                                                                                                                                                      KASDLPQSGDQVN-----KDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSES 233
                                                                                                                                                                                                                                                                                                                                  NGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVFGLY-----QQLLQSSSSAAVDI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKVAVEVI------KNLLTNTLVLDLLG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DITCK------YRTILDSTVVASQREYI------NSVKQGKP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKSYVYPEIKFPEI---SDLLFFNLTGSIFPTSDKKHIVVSPVMLTMAESLSQSPADSLS 567
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                                                                                                                                                                                                                                                                                     -----DVIENSCDPVLDLHMSLEELYTQNLLQRQDENTPSV 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Mismatches 147; Indels 81; Gaps
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RESULT 11
PCT-US93-11298-2
; Sequence 2, Application PC/TUS9311298
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHOD OF CON
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US-07-989-845-2
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APPLICANT: Bass, Steven
APPLICANT: Swartz, James
TITLE OF INVENTION: METHO
TITLE OF INVENTION: PRODI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,8
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                      269 NLCDEKOKVAVEVIKNLLINTLYLDLLGLGLTLPANKNGIA 309
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                                                                                                                                                                                                                                                                                                                                                                   160 VFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINS--- 216
                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
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                                                                                                                                                                                                                                                                                     VKQGKPISNYYVGY----SESMCEIKDIIRDQQYNVQLIGTSD---KPYVYTDVLALNS 268
                                                                                                                                                                                                                                                                                                                              --GGVKQIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL 118
                                                                                                                                                                     -----KVNEEWKNNVGTGSTVKWPIGLG---GKGNDGIA 206
                                                                                                                                                                                                                                               VLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLA---
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415/952-9881
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O Point San Bruno
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    h, Inc.
METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION IN BACTERIAL CELLS
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

STREET: CITY: S

T: 460 Point San Bruno South San Francisco

Blvd

ADDRESSEE:

Genentech,

TITLE OF INVENTION:

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US-09-204-208A-11
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                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 11, Application US/09204208A Patent No. 6399320
APPLICANT: Ebenbichler, Christine
APPLICANT: Achhammer, Gunthar
APPLICANT: Ankenbauer, Waltraud
TITLE OF INVENTION: Modified DNA-Polymerase from Carboxydothermus hydrogenoformans an
TITLE OF INVENTION: use for Coupled Reverse Transcription and Polymerase Chain React
FILE REFERENCE: 4765
CURRENT APPLICATION NUMBER: US/09/204,208A
CURRENT FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: EP/97121151.1
                                                                                                                                                                   APPLICANT: Markau, Ursula
APPLICANT: Ebenbichler, (
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LENGTH: 348 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION: 415/225-1896
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 VSSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFT 159
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nes 52; Conserv
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COMPUTER: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                     -----KVNEEWKNNVGTGSTVKWPIGLG---GKGNDGIA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKQGKPISNYYVGY----SESMCEIKDIIRDQQYNVQLIGTSD---KPYVYTDVLALNS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GGVKQIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL 118
                                                                                                                                                                                                                                                                                                                                                                                       NLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFAEASLTGAGATFPAPVYAKWA-----DTYQK----ETGNKVNYQGI------GSS--
                                                                                                                                                                                                                                                                                                                                                                                                                          VLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLA---
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910/371-7168
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23.5%; Pred. No. 1.2;
ative 42; Mismatches 7
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CURRENT APPLICATION NUMBER: US/09/269,861A
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: PCT/PP97/05391
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: EP/96115873.0
PRIOR APPLICATION NUMBER: EP/96115873.0
PRIOR FILING DATE: 1996-10-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PACENTIN VETSION 3.0
SEQ ID NO 8
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
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Patent No. 6400....
Patent INFORMATION:
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Best Local
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APPLICANT:
APPLICANT:
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                                                                                     Query Match
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bonch-Osmolovskaya, Elizaveta
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Carbooxydothermus hydrogenoformans
                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 4494
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                                                                                                                                           LENGTH: 831
TYPE: PRT
ORGANISM: Carboxydothermus hydrogenoformans
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 21 ENGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASL------QSLPDV-----FST
                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYGISDFGLGRDLKIPREVAGKYÍKNÝFANÝPKVRÉYLDÉLVRTAŘEKGÝVTTLFGR--R 501
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67; Conserv
                                                    h 5.1%; Score 92.5; DB 4; Similarity 19.5%; Pred. No. 5.1; 67; Conservative 52; Mismatches 110;
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Svetlichny, Vitaly
Schmitz-Agheguian,
                                                                                                                                                                                                                                                                                                                                                                                                                           Angerer, Bernhard
Ebenbichler, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reiser, Astrid
                                                                                                                                                                                                                                                                                                                                                                                                                     Laue, Frank
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19.5%; Pred. No. 3.
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                                                         Indels 115;
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US-08-639-501-2
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                                                                                                                                                                         APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
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APPLICANT: Tavtig
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                   TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION UDATA:
APPLICATION UMBER: US 08/585,391
FILING DATE: 11-JAN-1996
                                                                                                                                     APPLICATION NUMBER: US 08/573,779 FILING DATE: 18-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chromosome 13-1
TITLE OF INVENTION: Susceptibility
NUMBER OF SEQUENCES: 124
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                                                                             NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/639,501 FILING DATE: 29-APR-1996
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FOR SEQ ID NO:
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1201 New York Avenue N.W., Suite 1001
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Weber, Barbara
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RESULT 15
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                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 80.
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
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LENGTH: 3418 amino aci
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TITLE OF INVENTION: CHARACTERIZED BRCA1
TITLE OF INVENTION: PROTEINS AND SCREEN:
TITLE OF INVENTION: CHARACTERIZED BRCA1
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                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ---IFLPYLVSLGGVKSLDE------SLVRGV----TGDLHS-----FVSSS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 NGNEVKLINLIKD-----VLPTQVSGYNIEYTEFD----CYSDASLQSLPDVFSTDS 69
                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                             CITY:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIPKDOKSELINCSAOFEANAFEAP----LTFANAD 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AQLSQQFDAKESEVRVLRCVDFANKE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQAISGTSPVASSFQGIKKSIFRIRESPK-ETFNASFSGHMTDPNFKKETEASESGLEIH 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQG----KPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
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                                                                                                                                                                                                                                                                                                                                          NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                  E: ARLES A. TAYLOR, JR. SUITE 1401, UNIVERSITY TOWER, BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JETTON, THOMAS L.
JETTON, THOMAS L.
ROBINSON-BENION, CHERYL L.
THOMPSON, MARILYN E.
THOMPSON, MARILYN E.
THOMPSON, MARICAN E.
THOMPSON E.

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KING, MARY-CLAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
       20 FEB 1996
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21.7%; Pred. No. 49;
                                   US/08/603,753D
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US-08-603-753D-4
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SEQUENCE CHARACTERISTICS:
LENGTH: 3418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 17 JAN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
AUTHORS: WOOSter, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: BRCA2 protein
LCCATION: 1 to 3418; Genbank locus HSU43746
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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L Local Similarity
Ches 86; Conserv
271 --CDEKQ-KVAVEVIKN------LLTNTLVLDLLGIGLTLPANKNGIAHLAKSSNFY--- 318
                                                                                                                                                                                                                                      439
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                                                                                                                                                                                                                                                                                                                                                                                                                                     104 ASVNGSVYGFPQYLC--SNFLLSSPNGTQ-QASSLLELA---QKVGYEQIVYPDVASSSS 157
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DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 789
DATE: 1995
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKKIF-----HEANADECEKSKNOVKEKYSFVSEVEPNDTDPLDSNVAHOKPFESGS 380
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                                                                                                                                                                                                                                   F-----LTSENSLP---RISSLPKSEKPLNEETVVNKRD--EEQHLESHTDCILAV 484
                                                                                                  KQAISGTSPVASSFQGIKKSIFRIRESPK-ETFNASFSGHMTDPNFKKETEASESGLEIH
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                                    -AQLSQQFDAKESEVRVLRCVDFANKE 344
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Search completed: January 24, 2003, 19:43:37 Job time : 25 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 ,
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. being printed, α

SUMMARIES

3 2 3 7 3 7 3 7 3 7 3 7 3 7 3 7 3 7 3 7		5.8 5.8 5.7 5.7 5.7	10182 10182 5024 511 511 511 753 761 397 4643 286	23 23 23 23 23 23	ABP38314 AABP38314 AAP81161 AAP81180 AAR07574 ABP29819 ABP29819 ABP39259 ABB71009 ABB71009 ABB53627	Staphylococcus epi S. epidermidis ope Recombinant alpha- Sequence of alpha- Alpha-amylase enco Streptococcus poly Streptococcus poly Streptococcus poly Staphylococcus poly Drosophila melanog Lactococcus lactis
••		Query				
	Score	Match	Match Length DB ID	BB	ID	Description
نسو	139.5	7.7	10182	23	ABP38314	Staphylococcus epi
ผ	138.5	7.7	5024	22	AAG82935	S. epidermidis ope
w	105.5	5.9	511	9	AAP81161	Recombinant alpha-
4	104.5	5.8	511	9	AAP81180	Sequence of alpha-
ۍ.	104.5	5.8	512	11	AAR07574	Alpha-amylase enco
o,	104	5. 8	753	23	ABP29819	Streptococcus poly
. 7	104	5. 8	761	23	ABP27624	Streptococcus poly
80	103.5	5.7	397	23	ABP39259	Staphylococcus epi
9	103.5	5.7	4643	22	ABB71609	Drosophila melanog
10	103	5.7	286	23	ABB53627	Lactococcus lactis

Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

4. U	44 9		42	41	40	39	38	37	36	35		33 9				29	28	27				23 9				19	18 9					13 10		
96	6.5	6.5									7.5	7.5	7.5	7.5	7.5	98			8.5	8.5	8.5	8.5	8.5	8.5	8.5		9.5					101.5 5		
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3 ABB49873		1 AAY79305	2 AAB30804	2 AAB70158	2 AAB65201	1 AAY66678		AAGE	3 AAU96176							AAG3573	AAG	AAG3															ABB7118	3 ABB90996
Listeria monocytog	Herbicidally activ	Plasmodium falcipa	Amino acid sequenc	r B	Human PRO1009 (UNQ	Membrane-bound pro	Human PRO1009 prot	Human AFP protein	Human secreted pro	Human albumin fusi	Human type 3 inosi	Protein containing	Amino acid sequenc	Staphylococcus epi	M. catarrhalis str	Zea mays protein f	Zea mays protein f	Zea mays protein f	Drosophila melanog	Protein containing	Protein containing	Protein containing	Lactococcus lactis	B.thuringiensis se	Coleoptera toxin f	Herbicidally activ	Herbicidally activ	pstS variant. Esc	H. pylori bacteria	obact		Listeria monocytog	Drosophila melanog	Herbicidally activ

ALIGNMENTS

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RESULT 1
ARB53814
ID ARB53814
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                                                                                                                       N-PSDB; ABN90859.
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08-NOV-1997;
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                                                                                                                                                                     WPI; 2002-381255/41.
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                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
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97US-064964P.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                          S. epidermidis open reading frame protein sequence SEQ ID NO:2964
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                                                                                                                         Staphylococcus epidermidis SR1 vaccination; endocarditis.
                                                       WO200134809-A2
                                                                                      Staphylococcus epidermidis
                                                                                                                                                                                                                 03-SEP-2001
                                                                                                                                                                                                                                                                                    AAG82935 standard; Protein; 5024 AA
                    17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLTLPANK----NGIAHLAKSSNFYAQLSQQFDAKESEVRVL------RCVDF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QQASATSSKTSENPATIEEVLGLSQAIYDTKNALNGEQRLATEKSKDLKLIKGLKDLNK 919:
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                                                                                                                                           strain;
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                                                                                                                                             infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in vaccination. The nucleic acids (I) may be used to produce the CC in vaccination. The nucleic acids (I) was the production of vectors CC s. epidermidis polypeptides (II) via the production of vectors CC containing them which are used to produce hosts cells which express the CC oblypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. CC the polypeptides may also be used to assay for other inhibitors of their CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA CC AAH55098 represent oligonucleotide sequences and primers which are used CC in the exemplification of the present invention. AAH55091 to CC AAH55098 represent oligonucleotide sequences and primers which are used CC in the exemplification of the present invention. CC sequences given in the sequence listing of the present specification, though sequences are given in the disclosure for SEQ ID NO:4445 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, CC consequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-316495/33.
N-PSDB; AAH53785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
---ANKEVKNCAGVL 352
                                                                                                                                                                             DQQYNVQLIGTSDKPYVYTDVLALNSNLCDEK-----QKVAVEVIKNLLTNTLVLDLLG 296
                                                                                                                                                                                                                         L----DNAMKDLRDTLES--NSTSVPNSVNYINADK-----NLQIEFDEAL-----
                                                                                                                                                                                                                                                             LPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSESMCEIKDIIR 242
                                                                                                                                                                                                                                                                                                      EDTKDALNGIQRLSKAKAKAIQYVQSLSYINDAQRHIAESNIHNSDDLSSLANTLSKASD
                                                                                                                                                                                                                                                                                                                                                SSSSTVFGLYQ-----
                                                                                                                                                                                                                                                                                                                                                                                    NNQAFPVQASSNYINSDEDLKQQFDHALSNARKVLAKENGKNLDEIQIEGLKQVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                            --YGFPQYLCSNFLLSSPNGTQQASSLLELAQKV------GYEQIVYPDVA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTAAKSKAEKLIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLRDEL 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFTQAINNARDAL-NKTQGQNLDFNAIDTFKD-----DIFKTKD-----ALNGIER 3971
                                                         AQLEDVTNKVNSANTLTELSQLTQSTLKLNDKMKLLRDKLKTLVNPVKASLNYRNADYNL
                                                                                                 LGLTLPANK----NGIAHLAKSSNFYAQLSQQFDAKESEVRVL-------RCVDF--
                                                                                                                                         -QQASATSSKTSENPATIEEVLGLSQAIYDTKNALNGEQRLATEKSKDLKLIKGLKDLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                    -QLLQS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 138.5; DB Pred. No. 0.075; 9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESLVRGVTGDLHSFVSSSASVNGSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140;
                                                                                                                                                                                                                                                                                                                                                    -----SSSAAVDIKASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 147;
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                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                         The sequence encoding the protein can be used to construct an expression vector for the prodn. of alpha amylase in yeast cells. The transformants and recombinant enzyme produced can be used in fermentation processes e.g in baking and brewing. The transformed yeasts are esp. suitable for prodn. of low carbohydrate beers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of amylolytic enzymes comprises use of recombinant having DNA from donor yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strasser A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schwanniomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP81161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HETB ) HEINEKEN TECHNISCH BEHEER BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1986;
  452
                           219
                                                    393
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                                                                                                                           146
                                                                                                                                                                           118
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                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                         18 SWNENGNEVKLINLIKDVLPTQ------VSGYNIEYTEFDCYSDASLQSLPDVFST 67
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                              YYELISKLNQIRNQAIKKDSAYST-YKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG
SQDITVSN--TGYS-SGDKVIDIISCNSVLAGDSGSLSVSISGRMPQVYAPSSVLS-GSG
                      -QGKPISNYYVGYSESMCEIKDIIR-----DQQYNVQLIGTSDKPYVYTDVLALNSN
                                                                                                                         QIVYPDVASSS-----FTVFG-----LY---QQLLQSSSSAA--
                                                                                                                                                CPYQNYMKGVTNYPLYYPVYRFFSDTSATSS--ELTSMISTLQSSCSDVSLLGNFIENHD
                                                                                                                                                                       C-----SNFLLSSP-----NGTQQASSLLELAQKV------GYE 145
                                                                                                                                                                                                 DNEVIGVFQTWVSDFVQNYSIDGLRIDSAKHVDTASLTKFEDASGVYNLGEVYQGDPTYT
                                                                                                                                                                                                                          DS----IFLPYLVSLGGVKSLD----ESLVRGVTGDLHSFVSSSASVN-GSVY-GFPQYL 117
                                                                                                                                                                                                                                                   AWNGDGSSVD----YSSFTPFNQQSYFHDYCLITNYNDQTNVEDCWEGDTEVSLPDLSTE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1988-057532/09.
DB; AAN81477.
                                                                        ASDLPQSGDQVNKDITQK---YRTILDSTVVASQREYINSVK----
                                                                                                QVRFPSVTSDTSLIKNDMAFIILGDGIPIIYYGQEQGLNGGSDPANREALWLSGYNTDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
                                                                                                                                                                                                                                                                                                                                                      511 AA;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yeast; brewing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86EP-0111586
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                                                                                                                                                                                                                                                                                                                5.9%;
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                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511
                                                                                                                                                                                                                                                                                                               Score 105.5; I
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by transformed microorganisms DNA technology to give transformed
                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                            DB 9;
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RESULT 4
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                                                                                                                                                                                                                        Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                         A cosmid library is constructed from genomic DNA of ATCC26076 and this screened for inserts contg. the AA gene by ability to transform S.cerevisiae GRF 18 to histidine prototrophy. One positive cosmid (32kb; pYcl) was digested with EcoRI, religated and used to transform E.coli JA221. Positive transformants contain pYcl-alpha, which includes a 5kb EcoRI fragment contg. the gene in AAN81525.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide prodn. from ceesp. coding alpha amylase starch to ethanol
                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Fig 2A-2C; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-078794/12.
N-PSDB; AAN81525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of alpha-amylase castellii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwanniomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brewing;
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             180
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ASDLPQSGDQVNKDITQK----YRTILDSTVVASQREYINSVK----
                                 ÓVRFPSVTSDTSLIKNDMAFIILGDGIPIIYYGQEQGLNGGSDPANREALWLSGYNTDSE 392
                                                                                                                                                                         AWNGDGSSVD----YSSFTPFNQQSYFHDYCLITNYNDQTNVEDCWEGDTEVSLPDLSTE
                                                                                                                                                                                               SWNENGNEVKLINLIKDVLPTQ------VSGYNIEYTEFDCYSDASLQSLPDVFST 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICNO
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                                                        OIVYPDVASSS-----
                                                                               CPYQNYMKGVTNYPLYYPVYRFFSDTSATSS--ELTSMISTLQSSCSDVSLLGNFIENHD 332
                                                                                                     C-----SNFLLSSP-----NGTQQASSLLELAQKV------GYE 145
                                                                                                                              DNEVIGVFQTWVSDFVQNYSIDGLRIDSAKHVDTASLTKFEDASGVYNLGEVYQGDPTYT 274
                                                                                                                                                  DS----IFLPYLVSLGGVKSLD----ESLVRGVTGDLHSFVSSSASVN-GSVY-GFPQYL 117
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273
                                                                                                                                                                                                                                                                     511 AA;
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87EP-0110370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           castellii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breadmaking;
                                                                                                                                                                                                                                                                                                                                                                                                            from cells transformed with yeast DNA amylase or glucoamylase, able to conve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                  5.8%;
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                                                        FTVFG----LY---QLLQSSSAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dohmen
                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biomass
                                                                                                                                                                                                                                  Score 104.5;
Pred. No. 2.3;
                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA
                                                                                                                                                                                                                                              DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Schwanniomyces
                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                       Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                              convert
                                                       -----VPIK 179
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 AAR07574 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwanniomyces yeast cells; expression cassette; alpha-amylase; marker gene; regulon; signal peptide; terminator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR07574;
                                                                                                               The expression cassette may contain a regulon (R), a signal peptide sequence (S), a foreign protein sequence (F) and a terminator (T) of which R and/or S and/or T are derived from the alpha-amylase gene of S. occidentalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwanniomyces occidentalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marker gene; regulon; sig
autonomously replicating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1991
                                                                                                                                                                                                   Transformed Schwanniomyces yeast cells - cassette contg. regulon, DNA coding for
                                                                                                                                                                                                                                                                                                                                                                        EP394538-A.
                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                           S contains all or part of one of the sequences represented in AAQ06383-87.
F is e.g. a cellulase, interleukin, insulin-like-growth fa
                                                                                                                                                                    Disclosure; Fig 1B(1-6); 59pp; English
                                                                                                                                                                                                  cassette contg. regulon,
                                                                                                                                                                                                                                  N-PSDB; AAQ06388
                                                                                                                                                                                                                                             WPI; 1990-328670/44.
                                                                                                                                                                                                                                                                                                         28-APR-1989;
                                                                                                                                                                                                                                                                                                                              28-APR-1989;
                                                                                                                                                                                                                                                                                                                                                   31-OCT-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393
 See
                  MY1 acts as selective
                                                                                                                                                                                                                                                                 Hollenberg C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
          cassette
                                                                                                                                                                                                                                                                                      (RHEI ) RHEIN
                             interferon etc.
T is pref. all or part
(bp 1537-1740).
also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYELISKLNQIRNQAIKKDSAYST-YKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQDITVSN--TGYS-SGDKVIDII---SCNSVLAGDSGSLSVSISGGMPQVYAPSSVLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGICNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNLCDE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QGKPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDK---
                                                                                                      f. a 1.8
 AAQ06389
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276..319
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186..200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              /note="4"
                                                                                                      kb BglII-XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                         of
f
                    marker for the vector carrying the expression
                                                             interleukin, insulin-like-growth factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                         the terminator
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                                                                                                       fragment (bases
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foreign
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                                                                                                                                                                                                   an expression protein and
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                                         sequence
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                                                                                                                            alpha-amylase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus agalactiae
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
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                                                                          WPI; 2002-352536/38
N-PSDB; ABN70450.
                                                                                                                                                Telford J,
Tettelin H;
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80; Conserv
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Pred. No. 2.3;
48; Mismatches
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Best Local :
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27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
                                                                                                                                                                                                   group A streptococcus; Strept antiinflammatory; infection;
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                                                        29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                   Streptococcus agalactiae
                                                                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 4424.
                                                                                                                                                                                                                                                                                                                      02-JUL-2002 (first entry)
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59; Conserv
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-352536/38
N-PSDB; ABN68255.
                                                                   24-JUL-2002
                                                                                                      ABP39259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                        ABP39259 standard;
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                                                                                                                                                                                                                                                                  NFYAQLSQQFDAKESEV 332
                                                                                                                                                                                                                                                                                                     PYVPQVIMTTTSNVLMPQKQ---VEKVKLLTPFTI----
                                                                                                                                                                                                                                                                                                                                     PYVYTDVLALNSN-LCDEKOKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSS 315
                                                                                                                                                                                                                                                                                                                                                                            TKSYSKKELVNA-ELTKVISN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLLQSSSSAAVDIKAS-----DLPQSGD-------QVNKDITQKYRTILDS
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23.0%;
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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

Staphylococcus epidermidis ORF amino acid sequence SEQ ID

NO:4104.

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RESULT
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Best Local Similarity
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a polypeptide, useful for diagnosing and
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08-NOV-1997;
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                                                                                                                                                FYAQLSQQFDAKESEVRVLRCVDFANKEVKNCAGVLRPF 355
                                                                                                                                                                                                                                                              LNSNLCDEK-----QKVAVEVIKNLLTNTLVLDLLG-LGLTLPANKNGIAHLAKSSN 316
                                                                                                                                                                                                                                                                                                                                                                         NYYVGYS---ESMCEIKDIIRDQQYNVQLIGTSDKP---
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                                                                                            -VSELAKRIDLTTQHYNELDHI----IENSKDTLKQF
                                                                                                                                                                                                                                                                                                                  EYEKGYDLLLESIRLIQEDLRQLNYDVHIYGSGSKKTSLVDFINQYHLNDLIKIYEPTQE
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Pred. No. 1.9;
72; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
3723
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                               specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072). This patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
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SHRKTFMRSIR----
                      SQRE-YINSVKQGKPISNYYVGYSESMCEIKDIIR-----
                                                                                                GAFIGKVHASDQDKYDELNFSLVSGPDDMYQSSKLFNISNNTGK---IYAISNLDIGLYK 3676
                                                                                                                     ASVNGSVYGFPQ--YLCSNF-LLSSPNGTQQASSLLELAQKVGYEQIVYP----DV----
                                                                                                                                               TPPLYSDA
                                                                                                                                                                                               NTTPYTFDI ----
                                                                                                                                                                                                                    STOPKTLTVGLFPYLPSWNENGNEVKLINLIKDVLPTQVSGYN-----IEYTEFD--
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                                                LNVSVSDGKFHVFSI----
                                                                                                                                                                       ---CYSDASLQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVSS----S
                                                                      ----ASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JC,
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                                                                                                                                                                                                                                                                                              4643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                               -----RSGNEGGLFRLEQDGSLRTASRFNHNLQDEFVIQVRVFDNG 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                        5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biology; cell signalling; insecticide;
                                                                                                                                                                                                                                               50;
-NIMRCRQKDVILITLQSDYQKASQHAVGNRRARSIDS
                                                                                                                                                                                                                                            Score 103.5;
Pred. No. 70;
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4643
                                                                                                                                                -WVV----VKIIEESQYPPIVTPLEVTINSFEDDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers
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                                                VKINVELVTNDMLKESVVIRFRRISASEFLL
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                                                                                                                                                                                                                                                                      DΒ
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                        .----DQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
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and c
                                                                                                                                                                                                                                               135;
                                                                                                                                                                                                                                                                       4643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 or more cell-cell
                                                                                                                                                                                                                                              Gaps
 3770
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                                                                                                                                                3619
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ABB53627
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                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 [published 18-OCT-2001] which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3820
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleotide sequence useful in lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolotine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis protein plpD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3771 DLNVVFAVRKQQIIPDSDEFFTSDEI----RQTLIDKKNEIENE-----TNLVVEDV--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001
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  197
                                                        155
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                                                                                  71
                                                                                                              99
                                                                                                                                       13 FPYLPSWNE--NGNEVKLINLIKDVLPTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSI
                                                                                                                                                                                   Local Similarity
                         QASSILELAQKV-GYEQIVYPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQ 189
TPRALDSVAAAVINYNFAISAKISEKES----IYQEPLNEDSAQWINFIAANQSDKNNK
                                                                                                             YAYLKSWNKANNGNIVS----IGDTIITPIHLYSTKYKNVTEIPDKSTIAIPNDVTNESR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTCQSNKNDCVH 3832
                                                                                 FLPYLVSLGGVKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPQYLCSNFLLSSPNGTQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLTLPANKNGIAH 310
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 329; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 286
                                                                                                                                                                                                                             286 AA;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000FR-0004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGL
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                                                                                                                                                                                  5.7%;
20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renault P,
                                                                                                                                                                   41;
                                                                                                                                                                                Score 103; DB
Pred. No. 1.3;
                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlich
                                                                                                                                                                                               23;
                                                                                                                                                                   88;
                                                                                                                                                                                              Length
                                                                                                                                                                   Indels
                                                                                                                                                                   40;
                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                   (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 207; 261pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                            useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002
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                             170
 207
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 VASQREYINSVKQGKPISNYYVG----YSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTD
                                                                                                                                                                        AS
                            GSVPDLRGLSNLQELNLGGNKL---GPEVVPSLASNL------ITISLKNNSFGSK 216
                                                      --YPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTV
                                                                                    GPLPSQIIRLSSSLQSLN-----
                                                                                                              GDLHSFV---
                                                                                                                                          SSPSFKILCFNGHVTELTVTGNRTVKLPGRFSSDSLF-TVLTKLSNLKTL--SLVSLGIS 120
                                                                                                                                                                                                 SQAFSLTFLLFLFLLPSVSESQLISSESRTLLEIQKHLQYPPTLRSWSN--WTNF-CYLP
                                                                                                                                                                                                                           TOPKTLTVGLFPY-LPSWNEN---GNEVKLINLIKDVL---PTOVSGYNIEYTEFDCYSD
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                                                                                                                                                                                                                                                                                                                 B
                                                                                                             -SSSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIV-
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                                                                                                                                                                                                                                                      5.6%; Score 101.5;
25.9%; Pred. No. 7.2;
tive 48; Mismatches
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                                                                                                                                                                LQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVR-GVT
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                                                                                    LSSNFI -- SGNIPKEISSLKNLRSLVLANNLFN 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                     747;
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                                                        206
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RESULT 12
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                                                                                                                                       Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB71182 standard; Protein; 859
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter
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11-JUL-2000;
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                                     311
                                                                                      256
                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
          162 GLYQQLLQSSSSAAVDIKASDLPQSGDQVNK-----DITQKYRTILDSTVVASQR-EYI 214
                                                              102
                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPEQIKKLNKLQSLDLSSNKFTGSIPRFLLSLPSLQNLSLAQNL---LSGSLP-----
                                     ASWMSEQRWAGEPEVMC
                                                           SSASVNGSVYGFPQYLCSNFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTVF 161
                                                                                                           YNIEYTEFDC-YSDASLQSLPDVFSTDSIFLPYLVSLGGVKSLDESLVRGVTGDLHSFVS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-656860/75.
DB; ABL15285.
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                                                                                                                                                                                                                                                                                                                                                                                                  from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JС,
                                                                                                                                     . Similarity 77; Conserv
CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 40338; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-191637P
2000US-0614150
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                                                                                                                                                  5.6%;
22.5%;
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                                    -----TIQHKSIAQEAYK-NY-----TITTSAVC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent
for elucidating co
                                                                                                                                     46;
                                                                                                                                   Score 101.5; I
Pred. No. 8.9;
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    elucidating cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                  No. 8.9;
                                                                                     -LRFTASTSTPKSGSKIAKR--
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                                                                                                                                     150;
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                                                                                                                                                              22;
                                                                                                                                                                                                                          format directly from
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                                                                                                                                                              Length
                                                                                     -GKKHPEPV 310
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                                                                                                                                                                                                                                                                                                                                                                                                                 1000
                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                     cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                 or more
                                                                                                                                    Gaps
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                                                                          The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate I. monocytogenes are expression and cell replication.
                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
            and modulate L. monocytogenes-related diseases. In addition, the sequence and proteins encoded by it are useful in pharmaceutical vaccines compositions for the treatment or prevention of infection monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                              Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Kose
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                                                                                                                                                                                                                                                                                                                                           mic sequence for Listeria monocytogenes, useful e.g. for prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                2002-010914/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLLVVVLDHKQSSVRALALRALATLCCAPQAINQLGSCGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLITLRLIFERLVRVLVISIEQSQCDLLLRANINMVATLMNIDYDGFASLSDAFVQNEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKVAVEVIKNLLTNTLVLDL--LGLGLTLPANKNGIAHLAK-SSNFYAQLSQQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSVKQGKPISNYYVGYSESMCEIKDIIRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEK
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 sequence data
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         The pstS gene encodes a phosphate-binding periplasmic protein that is part of the high-affinity phosphate transport system mediating phosphate uptake in certain prokaryotes such as E. coli. Gene expression is induced by phosphate starvation and positively regulated by the phosp protein. When phosphate levels in the surrounding medium are high the PstS gene product acts a repressor. PstS variants are molecules which have been modified
                                                                                                                                                                                                                                                                                                                                                                                     Phosphate; phosphate binding protein; transport; repressor; polypeptide synthesis; protein synthesis; metabolism; Escherichia coli; pstS; phoB; induction; repression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1027
 'n
                                                                                                                Claim 1; ; 58pp; English.
                                                                                                                                                        Nucleic
                                                                                                                                                                              WPI; 1994-126409/15
                                                                                                                                                                                                        Bass S,
                                                                                                                                                                                                                                                          20-NOV-1992;
                                                                                                                                                                                                                                                                                 20-NOV-1992;
                                                                                                                                                                                                                                                                                                                                     US5304472-A
                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                         pstS variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 DCYSDASLQSLPDVFSTDSIFLPYLV----SLGG-----VKSLDES------LVRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVVASQREYINSVKQGKPISNYYVGYSESMCEIKDIIRDQQYNVQL-IGTSDKPYVYTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILD-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAFVDAG-SAIKDAFNKDNYALTGTVEAFKOMGGEAEKTAKKTETSGKKIKDTLKLVEST 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKQTETTVSKSNQAIDTMLSGGVDQY--GNKL-----SEKTKSFLNSAKEL-YSQ--YQ 926
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                                                                                                                                     of.
                                                                                                                                                                                                                                GENENTECH INC
                                                                                                                                     acids encoding E. coli PstS protein variants - of polypeptide prodn. in Enterobacteriaceae ce
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                                                                                                                                                                                                        Swartz
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binding
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Pred. No. 26;
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RESULT 15
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Best Local
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                                                                                                                          01-APR-1997;
01-APR-1997;
                                   WPI; 1998-568251/48
N-PSDB; AAV07913.
                                                                                                                                                           31-MAR-1998;
                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                             therapy
                                                                                                                                                                                                                                                                                                                                                       GHPO 1516;
                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                   Al-Garawi A,
                                                                                          (INMR
                                                                                                                                                                                   08-OCT-1998.
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                        Helicobacter
                                                                                                                                                                                                                                                                                                                                                                               Helicobacter
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                                                                                                                                                                                                        WO9843479-A1
                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW73024 standard; Protein;
                                                                                                      (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLCDEKOKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKQGKPISNYYVGY----SESMCEIKDIIRDQQYNVQLIGTSD----KPYVYTDVLALNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GGVKQIIANT----VDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFAEASLTGAGAGFPAPVYAKWA-----DTYQK----ETGNKVNYQGI-----GSS--
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                                                                                         HUMAN GENOME SCI INC
MERIEUX ORAVAX PASTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                       infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 AA;
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                                                                                                                                                                                                                                                                                                                      pylori.
                                                                                                                                                                                                                                                                                                                                                                             pylori
                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                    Kleanthous
                                                                                                                          97US-0834666.
97US-0831310.
                                                                                                                                                            98WO-US06421
                                                                                                                                                                                                                                          721
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                             /note= "encoded by NAT"
                                                                                                                                                                                                                                                                         /label= Sig_peptide
                                                                                                                                                                                                                                                  'label= Mat_protein
obacter polynucleotides prevention and treatmer
                                                                                                                                                                                                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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24.0%;
                                                                                          PASTEUR MERIEUX SERUMS
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                                                                    Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.6
2; Mismatches
                                                                   Lissolo L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                    Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
 used to develop of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                          ET VACCINS.
                                                                    ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                     Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
           products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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New isolated Helicobacter for the diagnosis, prevent

treatment

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CC polypeptide designated GHPO 1516. It was deduced from an isolated CC genomic DNA sequence (see AAW70913). The invention provides a family CC genomic DNA sequence (see AAW70913). The invention provides a family CC of 76 kDa Helicobacter polypeptides (see AAW73022-32), as well as a CR ABW73035), and also polypucleotides (see AAW73022-32), as well as a CC AAW73035), and also polynucleotides (see AAW73001, AAW07912-21 and CC AAW07963-64) encoding them, expression cassettes, and methods for CC producing the unprocessed or mature polypeptides in host cells. The CC polypeptides can be used in vaccination methods to prevent or treat Hb CC infection in a mammal. Methods and products of the invention allow CC treatment and prevention of gastroduodenal diseases associated with Hb CC infections, including acute, chronic, and atrophic gastritis, and CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. Detection CC and diagnostic methods are also provided. GHPO 1516 was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 90-93; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections and gastroduodenal diseases
                                                                                                      378
  438 VTSNTWGAGCAYVGETISALTNSIAH-----
                                                                                                                                                        245
                                                                                                                                                                                                     324 EFSQVTSMIKNAQEIIAQSKIVSENAQNQNNLDTGKPFNPYTDASFAQSM-----LKNA 377
                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                   129 TQQASSLLELAQKVGYEQIV---YPDVASSSSFTVFGLYQQLLQSSSSAAVDIKASDLPQ 185
                                               287 -- TNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQLSQQFDAKESEVRVLRCVDFANK 343
                                                                                                                                                                                                                                                                                                                                                                                                            212 TADINGGVYQFCK--AKNGSSSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFDI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYY-VGYSESMCEIKDIIRDQ 244
                                                                                                 QYNVQLIGTSDKPYVYTDVLALNSNLCDE----KQKVAVEVIKNLL----- 286
                                                                                                                                                                                                                                                                                                      THRAEQLLINGAANI -- MQVLNTQCPLVRSTNNENTPGGGQPWGLSTSGNACSI ----FQQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%; Score 100.5; DB 19;
21.1%; Pred. No. 8.8;
vative 43; Mismatches 112;
-- FGTQEQQIQQAENIADTL--VNFKSR 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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